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Biochemistry 39:10799-10805(2000)
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DISULFID
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     TISSUE-Pancreas, and Spleen;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Astaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B.B., Bangner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B.B., Bardener C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Astapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Aniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Muhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Menterfield A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 20-32, IDENTIFICATION OF HCC-1(3-74) AND HCC-1(4-74), MASS SPECTROMETRY, AND CABBOHYDRATE-LINKAGE SITE SER-26.
PubMed-10978165; DOI=10.1021/Pi924888;
Richter R., Schulz-Knappe P., John H., Forsemann W.-G.;
"Posttranslationally processed forms of the human chemokine HCC-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                          016627; 013954;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Small inducible cytokine Al4 precursor (CCL14) (Chemokine CC-1/CC-3)
(HCC-1/HCC-3) (HCC-1(1-74)) (NCC-2) [Contains: HCC-1(3-74); HCC-1(4-74)].
N4); HCC-1(9-74)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pardigol A., Forsmann U., Zucht H.-D., Loetscher P., Schulz-Knappe P., Baggiolini M., Forssmann W.-G., Maegert H.-J.; McC-2, a human chemokine: gene structure, expression pattern, and biological activity."; Proc. Natl. Acad. Sci. U.S.A. 95:6308-6313(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99228475; PubMed=10213461; DOI=10.1089/107999099314153; Nomiyama H., Fukuda S., Iio M., Tanase S., Miura R., Yoshie O.; Organization of the chemokine gene cluster on human chromosome 17q11.2 containing the genes for CC chemokine MPIF-1, HCC-2, LEC, RANTES.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Bone marrow;

MEDINE=Bols 64136773; PubMed=8551235;
Schulz-Knappe P., Maegert H.-J., Dewald B., Meyer M., Cetin Y., Schulz-Knappe P., Maegert H.-J., Dewald B., Mayer M., Adermann K., Kubbies M., Tomeczkowski J., Kirchhoff K., Raida M., Adermann K., Kist A., Reinecke M., Sillard R., Pardigol A., Uguccioni M., Baggiolini M., Forssmann W.-G.;
"HCC-1, a novel chemokine from human plasma.";
J. Exp. Med. 183:295-299(1996).
                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98263352; PubMed=9600961; DOI=10.1073/pnas.95.11.6308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interferon Cytokine Res. 19:227-234 (1999).
                                                                              93 AA.
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                                                                              STANDARD;
                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
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                                                       SY14 HUMAN
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                               anti-HIV properties.";

5. Exp. Med. 192:1051-1058(2000).

-1- FUNCTION: Has weak activities on human monocytes and acts via receptors that also recognize MIP-1 alpha. It induced intracellular Ca(2+) changes and enzyme release, but no chemotaxis, at concentrations of 100-1,000 nM, and was inactive on T lymphocytes, neutrophils, and esolnophil leukocytes. Enhances the proliferation of CD34 myeloid progenitor cells. The processed form HCC-1(9-74) is a chemotactic factor that attracts monocytes esolnophils, and T-cells and is a ligand for CCR1, CCR3 and CCR5.

-!- SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                         "Natural proteclytic processing of hemofiltrate CC chemokine 1 generates a potent CC chemokine receptor (CCR)1 and CCR5 agonist with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
SEQUENCE OF 20-48, IDENTIFICATION OF HCC-1(9-74), MASS SPECTROMETRY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s; TAS.
cell proliferation; TAS.
                                                                                                                                                  Detheux M., Staendker L., Vakili J., Muench J., Forssmann U., Adermann K., Poehlmann S., Vassart G., Kirchhoff F., Parmentier Forssmann W.-G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00472; SMALL CYTOKINES CC; 1.
Alternative splicing; Cytokine; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Small inducible cytokine A14.
HCC-1(3-74).
HCC-1(4-74).
HCC-1(9-74).
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GO; GO:0004871; F:signal transducer activity; TAS.
GO; GO:0006874; P:calcium ion homeostasis; TAS.
GO; GO:000884; P:positive regulation of cell proli
InterPro; IPR000827; CC. chemkine sml.
InterPro; IPR001911; Chemokine ILB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
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EMBL; Z70292; CAA94307.1; -.
EMBL; Z70293; CAA94309.1; -.
EMBL; Z49269; CAA89263.1; -.
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MIM; 601392; -.
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                                                                                                                 PubMed=11085751;
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NCBI_TaxID=9031;
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G90826; Q910029;
01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Small inducible cytokine A4 homolog precursor (Macrophage inflammatory protein 1-beta homolog).
Name=CCL4; Synonyms=SCYA4;
Gallus gallus (Chicken).
                                                                                                                                                                                                                         1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYETNSOCS
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By similarity.
O-linked (GalNhc. . .).
R -> QTGGKPKVVKIQLKLVG (in isoform HCC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875; Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.; "Molecular cloning and sequencing of 25 different rhesus macaque chemokine cDNAs reveals evolutionary conservation among C, CC, CXC, AND CX3C families of chemokines."; Cytokine 18:140-148(2002).

BMBL; AF449266; AAA76070.1; -. HSSP; P10147; 1B50.

GO: GO:00065576; C:extracellular; IEA.

GO: GO:0006555; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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                                                                                                                                          Length 93;
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                                                                                                                                                                                 0; Indels
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PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 92 AA; 10120 MW; 021GAA371143D12A CRC64;
                                                                             /FTId=VSP 001060.
DDDB899DC9148836 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                          100.0%; Score 93; DB 1; I 100.0%; Pred. No. 4.9e-94;
                                                                                                                                                                                                                                                                                                                          61 KPGIVFITKRGHSVCTNPSDKWVODYIKDMKEN 93
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InterPro; IPR001811; Chemokine_IL8
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Macaca mulatta (Rhesus macaque).
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Best Local Similarity 100.
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DISULFID
CARBOHYD
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                             MEDLINE=95369710; PubMed=7642115; DOI=10.1016/0378-1119(95)00210-W; Pettrenko O., Ischenko I., Enrietto P.J.; "Isolation of a lovel chicken chemokine homologous to mammalian macrophage inflammatory protein-1 beta.";
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Petrenko O., Enrietto P.J.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Monokine with inflammatory and chemokinetic properties
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20049023; PubMed=10582310;
Hughes S., Bumstead N.;
"Mapping of the gene encoding a chicken homologue of the mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   By similarity.
Small inducible cytokine A4 homolog.
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Pred. No. 0.13;
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50AF9679A267408F CRC64;
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Last sequence update)
Last annotation update)
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By similarity.
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ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
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PROSITE; PS00472; SMALL CYTOKINES_CC; 1.
Chemotaxis; Cytokine; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ243034; CAB45103.1; -.
RSP; Pl3236; 1HW7; CC Chemkine sn
InterPro; IPR000827; CC Chemkine sn
InterPro; IPR001811; Chemokine_IE8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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56
72
87
9987 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.78;
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                                                                                                                                                                                                                                                                                     Gene 160:305-306(1995).
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                                                                                                                                                          TISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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tes 9; Conserv
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A SCHMILE 2.7. Ohme M., Suryobroto B., Zischler H.;

"The colugo (Cynocephalus variegatus, Dermoptera): the primates'
"The colugo (Cynocephalus variegatus)
"The colugo (Cynocephalus variegat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nester E.W.;
"The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.6%; Score 8; DB 2; Length 115;
100.0%; Pred. No. 2;
tive 0; Mismatches 0; Indels
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Complete proteome; Hypothetical protein.
SEQUENCE 267 AA; 28091 WW; CCDF37F1F6C84F6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein Atul591.
OrderedLocusNames=Atul591;
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.6%; Score 8; DB 2; Best Local Similarity 100.0%; Pred. No. 3.9; Matches 8; Conservative 0; Mismatches
                                             SEQUENCE FROM N.A.
MEDLINE=22337212; PubMed=12446821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 294:2317-2323(2001).
ERBL, AR009116; AAL42593.1; -.
PIR; AC2772; AC2772.
PIR; B97552; B97552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.00
Then 8; Conservative
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NCBI_TaxID=9457;
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Tsujimoto H., Iwabuchi S.;
Expression analysis of gene in canine atopic dermatitis.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB164618; BAD42447.1; -.
InterPro; IPR00181; Chemokine_IL8.
Fam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
SEQUENCE 92 AA; 10029 MW; 9D44596B37FD6910 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADH subunit 3.
Cynocephalus variegatus (Flying lemur).
Bukoryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Dermoptera; Cynocephalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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                                                                                       Hughes S.M., Bumstead N.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF146730, AAD48772.1; -.
HSSP; P13236; 1HUM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 90;
                                                                                                                                                                                      GO; GO: 0005576; C: extracellular; IEA.
GO; GO: 000809; P: chemokine activity; IEA.
GO; GO: 0006955; P: immune response; IEA.
GO; GO: 0006955; P: immune response; IEA.
InterPro; IPR00837; CC chemkine sml.
InterPro; IPR01811; Chemokine IDA.
SMART; SM00199; SCY; 1.
SEQUENCE 90 AA; 9986 MW; 50AF9679A2675ICB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                             9.7%; Score 9; DB 2;
100.0%; Pred. No. 0.13;
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8.6%; Score 8; DB 2
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 8; Conservative 0; Mismatches
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Matches 9; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 DYYETNSQC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 DYYETNSOC 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 SQCSKPGI 62
                                                                      SEQUENCE FROM N.A.
                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9615;
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QBHHAO;
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Q8HHA0
ID Q8HH
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AC Q8HH
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OG CYNO
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Gaps

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Length 326; Indels

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326 AA; 37371 MW; 998F71C5D8722C87 CRC64;
                                      8.6%; Score 8; DB 2;
100.0%; Pred. No. 4.6;
ative 0; Mismatches
                       Query Match
Best Local Similarity 100.
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                                                                                                                         11 FLLITIAL 18
                                                                                                                                                             37 FLLITIAL 44
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nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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  SEQUENCE
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Taniguchi K., Nishikawa K., Urasawa T., Urasawa S., Midthun K.,
Kapikian A.Z., Gorziglia M.;
"Complete nucleotide sequence of the gene encoding VP4 of a human rotavirus (strain K8) which has unique VP4 neutralization epitopes.";
J. Virol. 63:4101-4106(1989).
                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21608551; PubMed=11743194; DOI=10.1126/science.1066803; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Gelone sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens CSB.;
Science 294:3123-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human rotavirus II type 1.
Viruses; dsRNA viruses; Reoviridae; Rotavirus; Human rotavirus A;
Human rotavirus 2.
10.11_TaxID=36432;
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                                                                                                                                                                              AGR_C_2926p.
OrderedLocusNames=AGR_C_2926;
Grapcbacterium tumefaciens (Gtrain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae: Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 288
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IIICEAFPC; IRRO02781; DUF81.
PFdm; PF01925; DUF81; 1.
SEQUENCE 288 AA; 30488 MW; ZEBB853798BD14D7 CRC64;
                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 4.2;
tive 0; Mismatches
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                                                                                PRT;
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
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Best Local Similarity 100.
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GO; GO: 0004654; F:polyribonucleotide nucleotidyltransferase a. .; IEA.
GO; GO: 0003723; F:RNA binding; IEA.
GO; GO: 0016740; F:transferase activity; IEA.
GO; GO: 0016240; F:RNA processing; IEA.
InterPro; IPR001247; 3 ExoRNase.
InterPro; IPR004087; KH.
InterPro; IPR004089; KH.
InterPro; IPR000309; SI.
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                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
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                                                                                                                                                                                            Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
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PROSITE; PS50126; S1; 1.
Complete protensis, Nucleotidyltransferase; Transferase.
SEQUENCE 818 AA: 88221 MM; 1A57P962C413B17A CRC64;
  01-OCT-2003 (TrEMBLrel. 25, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)
Name=pnp; OrderedLocusNames=RB5804;
Rhodopirellula baltica.
Bacteria; Planter
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Last annotation update)
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100.0%; Pred. No.
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PRT;
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Pfam; PF01138; RNase PH; 2.
Pfam; PF0375; RNase PH C; 2.
SMART; SM0322; KH; 1.
SMART; SM0316; S1; 1.
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Best Local Similarity 100.0
Matches 7; Conservative
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                                                                                        MEDLINE-22074459; PubMed=12079558; DOI=10.1089/088922202760019329; MEDLINE-22074459; PubMed=12079558; DOI=10.1089/088922202760019329; MEDLINE-22074459; PubMed=12079558; DOI=10.1089/088922202760019329; MEDLINE-22074459; PubMed A.L., Wencharon R.M., Li P.L., American R.M.; Ruprecht R.M.; Roperent R.M.; Roperent R.M.; Respective transcriptorase chain reaction: variations in the reverse transcriptorase chain reaction: variations in the repression during chronic primate lentivirus infection."; RESE. AMN 6985-1; -... RESE. AMN 69809; Friemmune response; IEA. GO; GO:0006555; Primmune response; IEA. RESE. RESPONSE: Primmune response; IEA. InterPro; IPR000827; CC_chemkine_min.
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecidae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Length 56;
                                                                                                                                                                                                                                                                                                                                                                            56 AA; 6442 MW; EB12A0E0D41D6F68 CRC64;
Macrophage inflammatory protein 1 alpha (Fragment).
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Last annotation update)
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100.0%; Pred. No. 15;
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-ive 0; Mismatches
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PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
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SMART; SM00199; SCY; 1.
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Hunter M.G., Bawden L., Brotherton D., Craig S., Cribbes S., Czaplewski L.G., Dexter T.M., Drummond A.H., Gearing A.H., Heyworth C.M., Lord B.I., Mccourt M., Varley P.G., Wood L.M., Edwarda R.M., Lewis P.J., Belwarda R.M., Lewis P.J., 1 alpha with improved pharmaceutical properties."; Blood 86:4400-4408(1995).
                                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
protein 1-alpha) (MIP-1-alpha) (Tonsillar lymphocyte LD78 alpha
protein) (GO/G1 switch regulatory protein 19-1) (GOS19-1 protein)
(SIS-beta) (PAT 464.1) [Contains: MIP-1-alpha (4-69) (LD78-alpha (4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIJNE=91103879; PubMed=2271120;
Blum S., Forsdyke R.E., Forsdyke D.R.;
"Three human homologs of a murine gene encoding an inhibitor of stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89140347; PubMed-2521882;
Zipfel P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.;
Zipfenic activation of human T cells induces two closely related
genes which share structural similarities with a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-86223879; PubMed-3086300;
Obaru K., Fukuda M., Maeda S., Shimada K.;
"A cDNA clone used to study mRNA inducible in human tonsillar
Jymphocytes by a tumor promoter.";
J. Biochem. 99:885-894(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jang J.S., Kim B.E.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                     92 AA.
                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=CCL3; Synonyms=G0S19-1, MIP1A, SCYA3;
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  Pred. No.
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  100.0%;
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                              Conservative
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                                                                                 LLITIAL 18
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda, Chromadorea, Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 68 AA; 7893 MW; 5DF6271284D43973 CRC64;
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Pred. No. 17;
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WormBase; WBGene00008002; C38C10.6.
WormPep; C38C10.6; CE34740.
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MEDLINE=21098486; PubMed=11173868;
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100.0%; Pre
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                Hypothetical protein C38C10.6.
ORFNames=C38C10.6;
                                                                                                                                                                                    01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
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Science 282:2012-2018(1998)
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7; Conserve
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42 LLITIAL 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pubmed=10347159; DOI=10.1074/jbc.274.23.16077; Czaplewski L.G., McKeating J., Craven C.J., Higgins L.D., Appay V., Brown A., Dudgeon T., Howard L.A., Meyers T., Owen J., Palan S.R., Tan P., Wilson G., Woods N.R., Heyworth C.M., Lord B.I., Palan S.R., Evans P., Gilbert R., Craig S., Cribbes S., Edwards R.M., Evans S.J., Gilbert R., Morgan P., Eliot Randle E., Schofield N., Varley P.G., Fisher J., Jonathan P., Waltho J.P., Hunter M.G., "Identification of amino acid residues critical for aggregation of human CC chemokines macrophage inflammatory protein (MIP)-1alpha, MIP-lbeta, and RANTES. Characterization of active disaggregated chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variants...,
J. Binds. Locken. 274:16077-16084(1999).

1 Biol. Chem. 274:16077-16084(1999).

1 Biol. Chem. 274:16077-16084(1999).

2 Biol. Chem. 274:16077-16084(1999).

Binds to CCRI, CCR4 and CCRE. One of the major HIV-suppressive factors produced by CD8+ T cells. Recombinant MIP-1-alpha induces a dose-dependent inhibition of different strains of HIV-1, HIV-2, and simian immunodeficiency virus (SIV).

1- SUBUNIT: Self-associates. Also heterodimer of MIP-1-alpha(4-69) and MIP-1-beta(3-69).

1- SUBCELLUIAR LOCATION: Secreted.

1- INDUCTION: By TPA or PHA (TPA = 12-o-tetradecanoyl phorbol-13 acetate (tumor promoter); PHA = phytohemagglutinin (T-cell
                                                                                                                                                                                                                                                                                   SUBUNIT, AND INTERACTION WITH MIP-1-BETA(3-69).

PubMed=12070155; DOI=10.1074/jbc.M203077200;

Guan E., Wang J., Roderiquez G., Norcross M.A.;

"Natural truncation of the chemokine MIP-1beta /CCL4 affects receptor specificity but not anti-HIV-1 activity.";
J. Biol. Chem. 277:32348-32352(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                  Bertini R., Luini W., Sozzani S., Bottazzi B., Ruggiero P.,
Boraschi'D., Saggioro D., Chieco-Bianchi L., Proost P., van Damme J.,
"Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major HIV-suppressive factors produced by CD8+ T cells."; Science 270:1811-1815(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: N-terminal processed form LD78-alpha(4-69) is produced by proteolytic cleavage after secretion from HTLV1-transformed T-
                                                                                                                                                                                              "Identification of MIP-1 alpha/LD78 as a monocyte chemoattractant released by the HTLV-I-transformed cell line MT4."; AIDS Res. Hum. Retroviruses 11:155-160(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE OF 24-92 BY NMR, AND MUTAGENESIS OF ASP-49 AND GLU-89.
                                                                                       SEQUENCE OF 27-51, AND IDENTIFICATION OF LD78-ALPHA (4-69)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=12401480; DOI=10.1016/S1359-6101(02)00045-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytokine Growth Factor Rev. 13:455-481 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Menten P., Wuyts A., Van Damme J.;
"Macrophage inflammatory protein-1.";
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PDB; 1B50; NMR; A/B=24-92.
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M. GO: 0006925; C:soluble fraction; TAS.

RO: GO:0006817; F:chemokine activity; TAS.

RO: GO:0006817; F:chemokine activity; TAS.

RO: GO:0006817; F:chemokine activity; TAS.

RO: GO:0006817; F:antimicrobial humoral response (sensu Verte. . .; TAS. RO: GO:0006818; P:call.cull signalling; TAS.

RO: GO:0006818; P:call.cull signalling; TAS.

RO: GO:0007267; P:call motility; TAS.

RO: GO:0007267; P:call motility; TAS.

RO: GO:0006918; P:chemotaxis; TAS.

RO: GO:0006918; P:chemotaxis; TAS.

RO: GO:0006918; P:chemotaxis; TAS.

RO: GO:0006918; P:chemotaxis; TAS.

RO: GO:0006918; P:inflammatory response; TAS.

RO: GO:0007165; P:inflammatory response; TAS.
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NCBI_TaxID=47573;
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10010: Improved pharmaceutical
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PROSITE; PS00472; SMALL CYTOKINES CC; 1.
3D-structure; Chemotaxis; Cytokine; Direct protein sequencing;
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MEDLINE=20330374; PubMed=10871400; DOI=10.1093/nar/28.13.2512;
Chesnick J.M., Goff M., Graham J., Ocampo C., Lang B.F., Self
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E->A: Reduces self-association
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00.0%; Pred. No. 22;
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tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inflammatory response; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chrysodidymus synuroideus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.5
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
Genew; HGNC:10627; CCL3.
MIM; 182283; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 AA;
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444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=rps19;
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DISULFID
MUTAGEN
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Name=nad3;
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                                                                                                                                                                                                              RESULT 18
Q6DUK4
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05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
protein L-alpha) (MIP-1-alpha).
Name=CCL3; Synonyms=SCYA3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Werling D.;
"Role of chemokines in RSV infection.";
"Role of chemokines in RSV infection.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Monokine with inflammatcory and chemokinetic properties.
Binds to CCR1, CCR4 and CCR5 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
-!- SIMILARITY: Belongs to the S19P family of ribosomal proteins.
EMBL; AF222718; AAF36954.1; -.
HSSP; P80381; 1QKF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Interrace
Interr
                                                                                              GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0001735; F:structural constituent of ribosome; IEA.
GO; GO:000412; P:protein biosynthesis; IEA.
InterPro; IPRO0222; Ribosomal S19.
PRINTS; PR00975; RIBOSOWALS19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5%; Score 7; DB 2; Length 92; 00.0%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.5%; Score 7; DB 1; Length 93; 100.0%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion, Ribonucleoprotein, Ribosomal protein. SEQUENCE 92 AA; 11031 MW; 4DDA141178B58C74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 AA
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InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_IL8.
                                                                                                                                                                                                                                                                                                                                        ProDom; PD001012; Ribosomal S19; 1.
PROSITE; PS00323; RIBOSOMAL_S19; 1.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AIPFFLL 13
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Best Local Similarity
Matches 7; Conserv
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Q8SQA6;
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SY03_BOVIN
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Gaps

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0; Indels

Conservative

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PubMed=1524836; DOI=10.1016/j.ympev.2004.05.003;

A Macey J.R., Papenfuss T.J., Kuehl J.V., Fourcade H.M., Boore J.L.;

Thylogenetic relationships among amphisbaenian reptiles based on complete mitochondrial genomic sequences.";

MOI: Phylogenet. Evol. 33.22-31(2004).

-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

-!- SIMILARITY: Belongs to the complex I subunit 3 family.

R EMBL; AY605474; AAT08510.1; -..

GO; GO:0005739; C:mitochondrion; IEA.

R InterPro; IPR000440; Oxidored_q4.

R Pfam; PF00507; Oxidored_q4.

R Mitochondrion; NAD; Oxidoreductase; Ubiquinone.

SEQUENCE 115 AA; 13186 MW; 088A852664ABFE01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gарв
                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Macrophage inflamatory protein 1 alpha.
Sus scrofa (Pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Amphisbaenia; Trogonophidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Stirling C.M.A., Takamatsu H.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY643423, AAT650711, --
GO, GO:000576; C:extracellular; IEA.
GO; GO:0006909; F:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR000827; CC chemkine sml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00048; IL8; 1. SMART; SM0199; SCY; 1. PROSITE; PS00427; SMALL CYTOKINES CC; 1. SEQUENCE 93 AA; 10117 MW; 088DZ6CAEE28414C CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%; Score 7; DB 2;
100.0%; Pred. No. 22;
tive 0; Mismatches
                                                                                                                                          93 AA
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25-0CT-2004 (TrEMBLrel. 28, Last seq
25-0CT-2004 (TrEMBLrel. 28, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.5
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                          PRELIMINARY;
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SQCSKPG 63
                                    SQCSKPG 62
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NCBI_TaxID=94420;
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12 LLITIAL 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10141;
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SY02 CAVPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-2268959; PubMed=12742752; DOI=10.1016/S1055-7903(02)00418-9;
MEDLINE-2268959; PubMed=12742752; DOI=10.1016/S1055-7903(02)00418-9;
Ishiguro N.B., Miya M., Nishida M.;
Ishiguro N.B., Miya M., Nishida M.;
Ishiguro E. Millian relationships: a mitogenomic perspective on the phylogenetic reality of the "Protacanthopterygii".";
Mol. Phylogenet. Evol. 27-476-488 (2003).

C. -I- SIMILARITY: Belongs to the complex I subunit 3 family.

EMBL; APO04107; BAC58219-1; -.

GO: GO: 0005739; C:mitochondrion; IEA.

GO: GO: 00016391; F:oxidoreductase activity; IEA.

GO: GO: 0016491; F:oxidoreductase activity; IEA.

GO: GO: 0016491; F:oxidoreductase activity; IEA.

GO: GO: 0016491; F:oxidoreductase activity; IEA.

Mitochondrion; NAD; Oxidored q4.

Mitochondrion; NAD; Oxidored q4.

Mitochondrion; NAD; Oxidored ceductase; Ubiquinone.

SEQUENCE 116 AA; 12920 MW; 63250CB6F286F276 CRC64;
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                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Argentiniformes; Platytroctidae; Platytroctes.
NCBI_TaxID=170202;
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Mammalia; Eutheria; Dermoptera; Cynocephalidae; Cynocephalus.
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Length 115;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADH dehydrogenase subunit 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.5%; Score 7; DB 2;
100.0%; Pred. No. 26;
7.5%; Score 7; DB 2;
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                                                                                                                                                                                                                                                 116 AA
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                     100.0%; Pred. No. 26; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cynocephalus variegatus (Flying lemur).
                                                                                                                                                                                                                                                                                                                                                                                                         Platytroctes apus (legless searsid).
                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2003 (TrEMBLrel. 25, NADH3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
nes 7; Conservative
                     Best Local Similarity 100.
Matches 7; Conservative
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                                                                                        12 LLITIAL 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion.
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Query Match
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08LX58
AC 08LX5
AC 08LX5
DT 01-0C
DT 01-0C
DT 01-0C
DF NADH3
GN NAMMED
OC BUKAZ
OC BUKAZ
OC BUKAZ
OC BUKAZ
OC RAMMED
OC NCBI
RR SEQUE
RR AATNAS
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AC 08500
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this eparament.
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Proc. Natl. Acad. Sci. U.S.A. 99:8151-8156(2002).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SIMILARITY: Balongs to the complex I subunit 3 family.
EMBL; AJ428849; CAD21800.2; -.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:00016491; F:OXIdoreductase (ubiquinone) activity; IEA.
GO; GO:0016491; F:OXIdoreductase activity; IEA.
GO; GO:0016491; F:OXIdoreductase activity; IEA.
GO; GO:0016491; F:OXIdored_Q4:
InterPro; IPR000440; OXIdored_Q4:
Fram; PPOSO7; OXIdored_Q4: I.
Mitochondrion; NAD; OXIdoreductase; Ubiquinone.
SEQUENCE 118 AA; 13382 MW; F6FE572039218C19 CRC64;
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-i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
Name=CCL2, Synonyms=MCP1, SCYA2;
Cavia porcellus (Guinea pio)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "CDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression of the recombinant protein.";
J. Immunol. 150:5025-5021(1993).
-i- FUNCTION: Chemotactic factor that attracts monocytes, but not
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Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
Pyrrolidone carboxylic acid; Signal.
SIGNAL 1 23 By similarity.
CHAIN 24 120 Small inducible cytokine A2.
MOD_RES 24 24 Pyrrolidone carboxylic acid (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.5%; Score 7; DB 2; Length 118;
100.0%; Pred. No. 26;
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InterPro; IPR001811; Chemokine_IL8.
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STRAIN=Z, TISSUE=Spleen;
MEDLINE=93267104; PubMed=8496603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L04985; AAA37047.1; -. PIR; I48147; I48147.
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Best Local Similarity 100.
Matches 7; Conservative
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STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
DOI=10.1128/JB.185.7.2330-2337.2003;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Evrland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-2154947; PubMed=11677608; DOI=10.1038/35101607;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C.M., Murgall N.L., Bentley S.D., Holden M.T.G., Sebaihia M., Barker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica servoar Typhi CT18.";
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                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
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EMBL; ALG67279; CAD09479.1; -.

EMBL; AE016845; AA070993-1; -.

GO; GO:0030528; F:transcription regulator activity; IEA.

GO; GO:0045449; P:regulation of transcription; IEA.
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Q82327; Q7C6P6; 01-WAR-2002 (TrEMBLrel. 20, Created) 01-WAR-2002 (TrEMBLrel. 20, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Putative regulatory protein. Name=rsD; OrderedLocusNames=STY3720, t3466; Salmoneila typhi.
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01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
1-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein B12F1.130.
Name=NCU03449.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 7.5%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 34; Matches 7; Conservative 0; Mismatches
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SEQUENCE 162 AA
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                                                                                                                                                                                                                                                                                            NCBI_TaxID=601;
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         SOW SERVICE SE
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-!- SIMILARITY: Belongs to the rsd/algQ family.
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MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                               Gapa
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Enterobacteriaceae; Salmonella.
By similarity.
N-linked (GlcNAc. . .) (Potential).
5905596851CF1C54 CRC64;
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Pfan; PF0453; Rsd_AlgQ.1.
3D-structure; Complete proteome; Transcription regulation.
SEQUENCE 162 AA: 18653 MW; 60A52C4D8B0142D8 CRC64;
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                                                                                                                                DB 1; Length 120
                                                                                                                                                                                               0; Indels
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16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Regulator of sigma D.
Name=rsd; OrderediocusNames=STM4165; ORFNames=STMF1.32;
Salmonella typhimurium.
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100.0%; Pred. No. 34;
tive 0; Mismatches
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                                                                                                                                                                 Pred. No. 27;
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                                                                                                                                              100.0%; Pred. ....
                                                                                                                             7.5%; Score 7;
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34 73 B
97 97 N
120 AA; 13741 MW;
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StyGene; SG????; rsd.
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Best Local Similarity 100.0
Then 7; Conservative
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Matches 7; Conservative
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DISULFID
CARBOHYD
SEQUENCE
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RESULT 24 Q82327 ID Q8

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101 SVAAIPF 107
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                                                                                                                                                                     HXC6 HUMAN
P09630;
                                                                                                                                              HXC6_HUMAN
                                                                                                               RESULT 27
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Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.; "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                              Nature 0:0-0(2003)
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR001254; Peptidase_S1.
PROSTIE; P800134; TRYPSIN_HIS; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 214 AA; 23078 MW; B3269D4996764ACO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.5%; Score 7; DB 2;
100.0%; Pred. No. 42;
tive 0; Mismatches
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Pred. No. 43;
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Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   preliminary data.
; AABX01000737; EAA27499.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABC transporter permease.
OrderedLocusNames=OB2099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TESSSRG 28
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QBEPKZ
IO QBEPKZ
IO QBEPK
AC QBEPK
AC QBEPK
AC QBEPK
AC OCCE
OC OCCE
OC BECT
OC CC
CC CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simeone A., Pannese M., Acampora D., D'Esposito M., Boncinelli E., "At least three human homeoboxes on chromosome 12 belong to the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90215256; PubMed=2576652;
MEDLINE=90215256; PubMed=2576652;
Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
Boncinelli E., Acampora D., Cafiero M., Faiella A., Simeone A.;
"Organization of human class I homeobox genes.";
Genome 31:45-756 (1989).
-!- FUNCTION: Sequence-specific transcription factor which is part a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
-!- SUBCELULLAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chariot A., Castronovo V., Le P., Gillet C., Sobel M.E., Gielen J., "Cloning and expression of a new HOXC6 transcript encoding a
                                                                                                                                                                                                                                                                             Simeone A., Mavilio F., Acampora D., Giampaolo A., Faiella A.,
Zappavigna V., D'Esposito M., Pannese M., Russo G., Boncinelli E.,
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                    Peschle C.;
"Two human homeobox genes, cl and c8: structure analysis and expression in embryonic development.";
Proc. Natl. Acad. Sci. U.S.A. 84:4914-4918(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P09630-2; Sequence=VSP 002392;
-!- SIMILARITY: Belongs to the Antp homeobox family.
-!- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                   01-MAX-1989 (Rel. 10, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Homeobox protein Hox-C6 (Hox-3C) (HHO.C8) (CP25)
Name-HOXC6; Synonyms=HOX3C;
235 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription unit.";
Nucleic Acids Res. 16:5379-5390(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=88262550; PubMed=2898768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=97024425; PubMed=8870653;
                                                                                                                                                                                                                                                            MEDLINE=87260899; PubMed=2885844;
                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
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EMBL; M16338; AAA36007.1; -.
PIR; B28030; WJHU3C.
HSSP; P02833; 9MT.
TRANSFAC; T01742; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repressing protein.";
Biochem. J. 319:91-97(1996)
STANDARD;
                                                                                                                                          Homo sapiens (Human).
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Gaps

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0; Indels

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Name=PRII;
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                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
Alternative splicing; Developmental protein; DNA-binding; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=92102952; PubMed=1684715; DOI=10.1016/0925-4773(91)90063-C;
Coletta P.L., Shimeld S.M., Chaudhuri C., Mueller U., Clarke J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE=94131843; PubMed=7905473;
Shimeld S.M., Gaunt S.J., Coletta P.L., Geada A.M., Sharpe P.T.;
"Spatial localisation of transcripts of the Hox-C6 gene.";
J. Anat. 183:515-523(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterisation of the murine \mbox{Hox-3.3} gene and its promoter.", Mech. Dev. 35:129-142\,(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kongsuwan K., Webb E., Housiaux P., Adams J.M.;
"Expression of multiple homeobox genes within diverse mammalian
                          MIM; 142972; -. Good of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poly-GIY.
Glu/Lys-rich.
Missing (in isoform 2).
FrId=VSP 002392.
M -> L (in Ref. 3).
W; BD68870347CB71C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antp-type hexapeptide Homeobox.
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01-JUL-1989 (Rel. 11, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-2004 (Rel. 44, Last annotation update)
Homeobox protein Hox-C6 (Hox-3.3) (Hox-6.1).
Name=Hoxc6; Synonyms=Hox-3.3, Hoxc-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuclear protein; Transcription regulation.
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MEDLINE=88329001; PubMed=2901346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26933 MW;
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EMBO J. 7:2131-2138(1988).
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Genew; HGNC:5128; HOXC6.
MIM; 142972; -.
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212
235
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235 AA;
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les 7; Conserv
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HXC6 MOUSE
DT 01-JUL
DT 01-JUL
DT 01-JUL
DT 01-JUL
DE Homeobo
GN Name=HO
GN Name=HO
CO Mammall
CO Ma
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Matches
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                                                                                                                                                                                                                                                              "Isolation and regional localization of the murine homeobox-containing gene Hox-3.3 to mouse chromosome region 15E."; Genomics 5:76-83(1989).
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PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00017; HOMEOBOX_2; 1.
PROSITE; PS0001; HOMEOBOX_2; 1.
Alternative splicing; Developmental protein; DNA-binding; Homeobox;
Nuclear protein; Transcription regulation.
SITE
                                                                                                                                                                                                                                                                                                                                                -I- FUNCTION: Sequence-specific transcription factor which is part a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
-I- SUBCELLULAR LOCATION: Nuclear.
MEDLINE-88328811; PubMed-2458223;
Sharpe P.T., Miller J.R., Evans E.P., Burtenshaw M.D., Gaunt S.J.;
"Isolation and expression of a new mouse homeobox gene.";
                                                                                                                                                                                                    Schughart K., Pravtcheva D., Newman M.S., Hunihan L.W., Jiang Z.,
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BD695C7347CB71C0 CRC64;
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Missing (in isoform PRI).
/FTId=VSP 002393.
AGGQ -> QQRP (in Ref. 3).
S -> N (in Ref. 4).
R -> A (in Ref. 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P10629-1; Sequence=Displayed;
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InterPro; IPR001356; Homeobox.
InterPro; IPR009057; Homeodomain_like.
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                                                                                                                                                   SEQUENCE OF 133-235 FROM N.A. MEDLINE=89357988; Pubmed=2570032;
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131 S
192 R
229 TE
26915 MW;
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PRINTS; PRO0024; HOMBGDBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                        Development 102:397-407(1988)
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TRANSFAC, T01744;
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Search completed: September 19, 2005, 08:47:20 Job time : 179 secs
   EMBL; AF017665; AAB94559.1; -.
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SEQUENCE FROM N.A.

STRAIN=C2A / ATCS 35395 / DSM 2834;

MEDLINE=21929760; PubMed=11932239;

MEDLINE=21929760; PubMed=11932239;

Allan N., Maylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Allan N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McKernan K., Talamas J., Tirrell A., Ye W.,

A inton L., McKernan F., McKernan K., Taramas D.A., Guss A.M.,

A ledgerich R., Ingram-Smitch C., Kuettner H.C., Krzycki J.A.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Rerry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,

Retry J.G., Jarrell K.F., Swanson R.V., Zinder S.H., Lander E.,

A Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

The genome of Methanosarcina acetivorans reveals extensive metabolic

Tand physiological diversity.";

EMBL, ABO10992; AAM06204.1; -.
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Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Boopterygota; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
Sphingidae; Sphinginae; Manduca.
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Four serine proteinases expressed in Manduca sexta haemocytes.";
Insect Mol. Biol. 8:39-53(1999)
-!- SIMILARITY: Belongs to peptidase family Sl.
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   DB 1;
7.5%; Score 7; DB 1;
100.0%; Pred. No. 45;
tive 0; Mismatches
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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Query Match 7.5
Best Local Similarity 100.
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GO; GO: 0004263; F: chymotrypsin activity; IEA.
GO; GO: 0004283; F: chymotrypsin activity; IEA.
GO; GO: 0004295; F: trypsin activity; IEA.
GO; GO: 0004295; F: trypsin activity; IEA.
GO; GO: 0004295; F: trypsin activity; IEA.
InterPro; IPR001234; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001203; Peptidase S1A.
InterPro; IPR001203; Peptidase S1A.
InterPro; IPR001203; PryP. SPC; II.
PROSITE; PS00134; TRYPSIN DOM; I.
PROSITE; PS00135; TRYPSIN SER; I.
PHOGOTE; PS00135; TRYPSIN SER; I.
PHOGOTE; PS00135; TRYPSIN SER; I.
PHOGOTE; PS00135; TRYPSIN SER; I.
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sigmodon hi
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sus scrofa
paralichthy
canis famil
macaca meme
equus cabal
macaca neme
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nomo sapien
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               SYOS MOUSE
SYOS HORSE
SY15 HUMAN
SYOS CANFA
SYOS CAVPO
Q8HYQ1
SYOS FELCA
SY16 HUMAN
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SYO5_BOVIN
SYO5_SIGHI
SY13_HUMAN
                                                                                                                                                                                                                                                                                                                     Q61VB4
Q8UK37
Q8UK37
Q8K477
SYQ9 MOUSE
Q64H35
SYZ6 HUMAN
Q67ZY4
SYZ4 MOUSE
REG1 BOVIN
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Q8QG56
Q98158
C07A RAT
Q8CGMS
SY02 RABIT
SY02 HUMAN
Q8V02 PIG
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SY02 HORSE
Q95N01
SY02 HORSE
SY02 MOUSE
COHYNS
SY17 HUMAN
EOTA HORSE
SY10 CANFA
SY10 CANFA
SY10 EOTA HORSE
SY10 BOVIN
QBJIM4
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SY10 HUMAN
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                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                           1612378 seqs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                                                                         September 19, 2005, 08:47:31
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Q8HYQ3
SY03 BOVIN
Q711P4
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SY04 RABIT
SY04 RAT
Q8HYQ2
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SY03_RAT
Q91ZL0
Q68A92
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SY04_CHICK
Q9PWA6
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SY04 HUMAN
Q6NSB0
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Q14745
Q14745
Q918E0
SY18 HUWAN
SY23 HUWAN
Q91Z65
Q91Z65
Q91YP8
SY05 RAT
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Q6DUK4
                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Result No.

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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

TISSUB=Pancreas, and Spleen;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahaksley J., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.M., Krzywinski M.I., Schlaka U., Smailus D.E.,

B. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 20-32, IDENTIFICATION OF HCC-1(3-74) AND HCC-1(4-74), MASS SPECTROMETRY, AND CARBOHYDRATE-LINKAGE SITE SER-26. Pubmed=10978165; DOI=10.1021/bi924848; Richter R., Schulz-Knappe P., John H., Forsemann W.-G.; Posttranslationally processed forms of the human chemokine HCC-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE=99228475; PubMed=10213461; DOI=10.1089/10799999314153; Nomlyama H., PubMed S., Tio M., Tanase S., Miura R., Yoshie O.; "Organization of the chemokine gene cluster on human chromosome 17q11.2 containing the genes for CC chemokine MPIF-1, HCC-2, LEC, and
                                      SY14 HUMAN STANDARD; PRT; 93 AA. 01657; 013954; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 05-UUL-2004 (Rel. 44, Last annotation update) 05-UUL-2011 inducible cytokine Al4 precursor (CCL14) (Chemokine CC-1/CC-3) (HCC-1/HCC-3) (HCC-1(1-74)) (NCC-2) [Contains: HCC-1(3-74); HCC-1(4-74)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pardigol A., Forssmann U., Zucht H.-D., Loetscher P.,
Schulz-Knappe P., Baggiolini M., Forssmann W.-G., Maegert H.-J.;
"HCC-2, a human chemokine: gene structure, expression pattern, and
                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                           TISSUE=Bone marrow;
MEDLINE=96136773; PubMed=8551235;
Schulz-Kappe P., Maegert H.-J., Dewald B., Meyer M., Cetin Y.,
Kubbies M., Tomeczkowski J., Kirchhoff K., Raida M., Adermann K.,
Kist A., Reinecke M., Sillard R., Pardigol A., Uguccioni M.,
Raggiolnin M., Forsemann W.-G.,
"HCC-1, a novel chemokine from human plasma.";
J. Exp. Med. 183:295-299(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98263352; PubMed=9600961; DOI=10.1073/pnas.95.11.6308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interferon Cytokine Res. 19:227-234(1999).
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 20-93.
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                                                                                                                                                                Name=CCL14; Synonyme=NCC2, SCYA14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biological activity.";
                                                                                                                                                                                   Homo sapiens (Human)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). anti-HIV properties. ". CIREMOALINE LECEPLOI (UCK) 1 and UCKS agonist with anti-HIV properties.";
J. Exp. Med. 192:1051-1058(2000).
-!- FUNCTION: Has weak activities on human monocytes and acts via receptors that also recognize MIP-1 alpha. It induced intracellular Ca(2+) changes and enzyme release, but no chemoteaxis, at concentrations of 100-1,000 nM, and was inactive on T lymphocytes, neutrophils, and eosinophil leukocytes. Enhances the proliferation of CD34 myeloid progenitor cells. The processed form HCC-1(9-74) is a chemotactic factor that attracts monocytes eosinophils, and T-cells and is a ligand for CCR1, CCR3 and CCR5.-!- SUBCELLULAR LOCATION: Secreted. TISSUE SPECIFICITY: Expressed constitutively in several normal tissues: spleen, liver, skeletal and heart muscle, gut, and bone marrow, present at high concentrations (1-80 nM) in plasma.

PTM: The Nrterminal processed forms HCC-1(3-74), HCC-1(4-74) and HCC-1(9-74) are produced in small amounts by proteolytic cleavage after secretion in blood.

PTM: HCC-1(1-74), but not HCC-1(3-74) and HCC-1(4-74), is partially 0-glycosylated; the 0-linked glycan consists of one GalagainAc disaccharide, further modified by two N-acetylneuraminic "Natural proteclytic processing of hemofiltrate CC chemokine 1 generates a potent CC chemokine receptor (CCR)1 and CCR5 agonist with -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family. SEQUENCE OF 20-48, IDENTIFICATION OF HCC-1(9-74), MASS SPECTROMETRY, s; TAS. cell proliferation; TAS Detheux M., Staendker L., Vakili J., Muench J., Forssmann U., Adermann K., Poehlmann S., Vassart G., Kirchhoff F., Parmentier Forssmann W.-G.; Small inducible cytokine A14. HCC-1(3-74). HCC-1(4-74). By similarity. PROSITE; PS00472; SMALL CYTOKINES CC; 1.
Alternative splicing; Cytokine; Direct protein sequencing; GO; GO:0004871; F:signal transducer activity; TAS. GO; GO:0006874; P:calcium ion homeostasis; TAS. GO; GO:0008284; P:positive regulation of cell proli InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_ILB.
PF00048; ILB; 1. Event=Alternative splicing; Named isoforms=2; MIM; 601392; -. GO; GO:0005615; C:extracellular space; TAS. IsoId=016627-2; Sequence=VSP_001060; IsoId=Q16627-1; Sequence=Displayed; Biochemistry 39:10799-10805(2000). EMBL; Z70292; CAA94307.1; -.
EMBL; Z7023; CAA94309.1; -.
EMBL; Z49269; CAA89263.1; -.
EMBL; AF088219; AAC63329.1; -.
EMBL; AF088219; AAF451965.1; -. EMBL; Z49270; CAA89264.1; -. Genew; HGNC:10612; CCL14. 933 Glycoprotein; Signal SIGNAL 1 HSSP; P13236; IHUM. PubMed=11085751; Name=HCC-1; Name=HCC-3 MIM; 601392; CHAIN DISULFID

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and mouse cDNA
                                                 TISSUE=Blood
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P16619; 096168;
01-AUG-1990 (Rel. 15, Last sequence update)
02-5-JAN-2005 (Rel. 46, Last annotation update)
Small inducible cytokine A3 like 1 precursor (Tonsillar lymphocyte LD78 beta protein) (LD78-beta(1-70)) (G0/G1 switch regulatory protein 19-2) (G0519-2 protein) (PAT 464.2) (Contains: LD78-beta(3-70); LD78-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
                                                                                                            1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYETNSQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYETNSQCS
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                    R -> QTGGKPKVVKIQLKLVG (in isoform HCC-
                                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Macrophage inflamatory protein 1 alpha.
Sus scrofa (Pig)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 51.3%; Score 258.5; DB 2; Length 93; Similarity 49.5%; Pred. No. 1.2e-21; 46; Conservative 22; Mismatches 24; Indels 1
                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                       Stirling C.M.A., Takamatsu H.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, ANG41423; AAT6507.1;
GO; GO:000575; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
InterPro; IPR001827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_IBB.
PF000489; IL8; 1.
                                                                     100.0%; Score 504; DB 1; Length 100.0%; Pred. No. 1e-49;
                                      /FTId=VSP 001060.
DDDB899DC9148836 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0B8D26CAEE28414C CRC64;
 By similarity.
O-linked (GalNAc.
                                                                                                                                                            61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
                                                                                                                                                  93
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                                                                                       0; Mismatches
                                                                                                                                                  61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN
                                                                                                                                                                                                                      93
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PSO0472; SMALL CYTOKINES CC; 1.
93 AA; 10117 MW; 0B8D26CAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=CCL3L1; Synonyms=G0S19-2, SCYA3L1;
                                                                                                                                                                                                                                          Created)
                                                 10678 MW;
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                                                                                        Conservative
                                                                                                                                                                                                                      PRELIMINARY;
  75
26
27
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Best Local Similarity
                                                                              Similarity
                                                 93 AA;
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9823;
  36
26
27
                                                                                                                                                                                                                                         25-OCT-2004
                                                                                        93;
DISULFID
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM
PROSITE;
                                                 SEQUENCE
                                                                    Query Match
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TO SY3L H
AC D163L H
DT 01-AUG-
DT 01-AUG-
DE LD78 b
DE LD78 b
DE beta (5-
CO N Name-CC
OS HOMO SE
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TISSUB-B-cell, Pancreas, and Spleen,

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

D. Matchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McKernan K.J., Male M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska N.,

Butterfield A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91103879; PubMed=2271120;
Blum S., Forsdyke R.E., Forsdyke D.R.;
"Three human homologs of a murine gene encoding an inhibitor of stem
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                         MEDLINE=90287702; PubMed=1972563;
Irving S.G., Zipfel P.F., Balke J., McBride O.W., Morton C.C.,
Bard P.R., Siebenlist U., Kelly K.;
"Two inflammatory mediator cytokine genes are closely linked and
variably amplified on chromosome 17q.";
Nucleic Acids Res. 18:3261-3270(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DENTIFICATION OF LD78-BETA(3-70) AND LD78-BETA(5-70), N-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PTM: The N-terminal processed forms LD78-beta(3-70) and LD78-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakao M., Nomiyama H., Shimada K.; "Structures of human genes coding for cytokine LD78 and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Cell. Biol. 10:3646-3658(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90287155; PubMed=1694014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein Sci. 13:2819-2824 (2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Cell Biol. 9:589-602(1990)
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                                                                            NCBI_TaxID=9606;
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Bovinae; Bos
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                  from peripheral blood monocytes. The cleavage to yield LD78-beta(3-70) is probably achieved by DPP4.
SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                                                                        HSSP; P10147; 1850.

R HSSP; P10147; 1850.

Genew; HGNC:10628; CCL3L1.

R H-InvDB; HIX0020418; -...

R H-InvDB; HIX00230418; -...

R H-InvDB; HIX00230418; -...

R GO; GO:0008009; F: Chemotian activity; NAS.

GO; GO:0008095; P: Chemotian activity; NAS.

GO; GO:0008095; P: Chemotian activity; NAS.

GO; GO:0008285; P: Chemotian activity; NAS.

R PROSITE; PS000472; SMALL CYTOKINES CC; 1.

R PROSITE; PS000472; SMALL CYTOKINES CC; 1.

R SIGNAL CHEMOTIAN ACTIVITY AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
peta(5-70) are produced by proteolytic cleavage after secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Small inducible cytokine A3 like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 240.5; DB 1; Length 93; Pred. No. 1.4e-19; 22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LD78-beta(3-70).
LD78-beta(5-70).
Cleavage (by DPP4) (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 By similarity.
74 By similarity.
91 L -> P (in Ref. 4; AAH07783).
10161 MW; A7A79E774006D61E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMK 91
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KPSVIFLTKRGRQVCADPSEEWVQKYVSDLB 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemokine CCL3/MIP-1ALPHA.
Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                        EMBL; X52149; CAA36397.1; -.
EMBL; M24110; AAA5859.1; -.
EMBL; D90145; BAA14173.1; -.
EMBL; BC07783; AAH07783.1; -.
EMBL; BC027888; AAH27888.1; -.
PIR; B35673; B35673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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28HYQ3
10 08HYQ3
AC 08HY
DT 01-M
DT 01-M
DT 01-M
DE Chem
OS Maca
OC Euka
OC Mamm
OX NCBI
RN [1]
RP SEQU
원
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory protein 1-alpha) (MIP-1-alpha).
Name=CCL3; Synonyms=SCYA3;
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Monokine with inflammatory and chemokinetic properties.
-!- FUNCTION: Monokine with inflammatory and chemokinetic properties.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                         Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
"Molecular cloning and sequencing of 25 different rhesus macaque
chemokine cDNAs reveals evolutionary conservation among C, CC, CXC,
AND CX3C families of chemokines.";
CYtokine 18:140-148(2002).
EMBL; AF449266; AAN76070.1; -.
MEDLINE=22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.4%; Score 239; DB 2; Length 92;
48.4%; Pred. No. 2e-19;
ive 21; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Small inducible cytokine A3.
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GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0006095; P:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR000827; CC chemkine sml.
InterPro; IPR001811; Chemokine IIB.
PRAM; PR00048; ILB; 1.
SMART; SM00199; SCY; 1.
SEQUENCE 92 AA; 10120 MW; 021GAA371143D12A CRC64;
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Pfam; PF00049; TL8; 1.

PROMIT; S000472; SMALL_CYTOKINES_CC; 1.

PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.

Chemotaxis; Cytokine; Inflammatory response; Signal.

24 By similarity.
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sapiens (Human)
                                                                                          FROM N.A.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=7537510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression.";
                                                                                           SEQUENCE
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                                                                                                                                                                      01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory protein 1-alpha) (MIP-1-alpha) (Tonsillar lymphocyte LD78 alpha protein) (G0/G1 switch regulatory protein 19-1) (G0S19-1 protein) (SIS-beta) (PAT 464.1) (Contains: MIP-1-alpha(4-69) (LD78-alpha(4-
                                                                                                                                                  MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                                                                            DB 1; Length 93;
                                                                                                             26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ortuno E., Rodriguez-Carreno M.P., Alonso F., Dominguez
Ezquerra A.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 92 AA; 10207 MW; AB1E0AESEA9F70E5 CRC64;
                     y similarity.
1266BFBFCEE5E8E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                      ; Score 238.5; DB 1
; Pred. No. 2.4e-19;
23; Mismatches 26
                                                                                                                                                                                                                             61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
                                                                                                                                                                                                                                                              KPGVIFQTKKGRQVCANPTEDWVQEYITDLELN 92
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 By similarity. By similarity.
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GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0008095; P:immune response; IEA.
InterPro; IPR001821; CC chemkine sml.
InterPro; IPR001811; Chēmokine_ILB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=CCL3; Synonyms=G0S19-1, MIP1A, SCYA3;
                                                                                                                                                                                                                                                                                                                                                              92
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                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                              PRT;
                                       10118 MW;
                                                                          47.3%;
                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ311717; CAC84398.1;
HSSP; P10147; 1B50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative MIP-1beta protein.
                                                                                                               43; Conservative
                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00048; IL8; 1.
                                                                        Query Match
Best Local Similarity
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Best Local Similarity
34
35
93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=MIP-1beta;
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P10147;
DISULFID
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                                     SEQUENCE
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ID SY03 HI
AC D104A7.

DT 01-MAR.

DT 25-JAN.

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DE protein
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DE (S
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SEQUENCE OF 24-92, AND MUTAGENESIS OF ASP-49.
MEDLINE=96127782; PubMed=8541527;
Hunter M.G., Bawden L., Brotherton D., Craig S., Cribbes S.,
Czaplewski L.G., Dexker T.M., Drummond A.H., Gearing A.H.,
Heyworth C.M., Lord B.I., Mccourt M., Varley P.G., Wood L.M.,
Edwards R.M., Lewis P.J.;
"BB-10010: an active variant of human macrophage inflammatory protein-
1 alpha with improved pharmaceutical properties.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT, AND INTERACTION WITH MIP-1-BETA(3-69).

PubMed=12070155; DOI=10.1074/jbc.M203077200;

Guan B., Wang J., Roderiquez G., Norcross M.A.;

"Natural truncation of the chemokine MIP-1beta /CCL4 affects receptor specificity but not anti-HIV-1 activity.";

J. Biol. Chem. 277:32348-32352(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bertini R., Luini W., Sozzani S., Bottazzi B., Ruggiero P.,
Boraschi D., Saggioro D., Chieco-Bianchi L., Proost P., van Damme J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDINE-21103879; PubMed=2271120; BEDLUM S., Forsdyke R.B., Forsdyke D.R.; "Three human homologs of a murine gene encoding an inhibitor of stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major HIV-suppressive factors produced by CD8+ T cells."; Science 270:1811-1815(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89140347; PubMed-2521882; Zipfel P. P., Balke J., Irving S.G., Kelly K., Siebenlist U.; Zipfel P. P., Balke J., Irving S.G., Kelly K., Siebenlist U.; "Mitogenic activation of human T cells induces two closely related genes which share structural similarities with a new family of
    Euteleostomí;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemoattractant
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                                                                                                                                                                                               MEDLINE-862233979; PubMed=3086300;
Obaru K., Fukuda M., Maeda S., Shimada K.;
"A cDNA clone used to study mRNA inducible in human tonsillar
Jymphocytes by a tumor promoter.";
J. Biochem. 99:885-894(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jang J.S., Kim B.E.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mantovani A.;
Identification of MIP-1 alpha/LD78 as a monocyte chreleased by the HTLV-1-transformed cell line MT4.";
AIDS Res. Hum. Retroviruses 11:155-160(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 27-40 AND 71-83, AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Cell. Biol. 10:3646-3658(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secreted factors.";
J. Immunol. 142:1582-1590(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell proliferation.";
DNA Cell Biol. 9:589-602(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 23-92 FROM N.A.
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3D-structure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0006928; P:calcium ion homeostasis; TAS.
GO:0006928; P:call motility; TAS.
GO:0006928; P:call motility; TAS.
GO:0006928; P:call motility; TAS.
GO:0006928; P:call-call signaling; TAS.
GO:0006935; P:chemotaxis; TAS.
GO:000710; P:cytoskeleton organization and biogenesis; TAS.
GO:000718; P:exocytosis; TAS.
GO:000718; P:cytoskeleton organization protein signalin. .; TAS.
GO:000659; P:inflammatory response; TAS.
GO:000659; P:regulation of viral genome replication; TAS.
GO:0007165; P:signal transduction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0005625; C:soluble fraction; TAS.
GO:0008009; F:chemokine activity; TAS.
GO:0004871; F:signal transducer activity; TAS.
GO:0004871; F:signal transducer activity; TAS.
GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.
                                                                                                           PubMed=10347159; DOI=10.1074/jbc.274.23.16077;
Czaplewski L.G., McKeating J., Craven C.J., Higgins L.D., Appay V.,
Brown A., Dudgeon T., Howard L.A., Meyers T., Owen J., Palan S.R.,
Tan P., Wilson G., Woods N.R., Heyworth C.M., Lord B.I.,
Brotherton D., Christison R., Craig S., Cribbes S., Edwards R.M.,
Evans S.J., Gilbert R., Morgan P., Eliot Randle E., Schofield N.,
Varley P.G., Fisher J., Jonathan P., Waltho J.P., Hunter M.G.,
"Identification of amino acid residues critical for aggregation of
human CC chemokines macrophage inflammatory protein (MIP)-lalpha, MIP-
lbeta, and RANTES. Characterization of active disaggregated chemokine
                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 274:16077-16084(1999).

-!- FUNCTION: Monokine with inflammatory and chemokinetic properties. Binds to CCR1, CCR4 and CCR5. One of the major HIV-suppressive factors produced by CD8+ T cells. Recombinant MIP-1-alpha induces a dose-dependent inhibition of different strains of HIV-1, HIV-2, and similan immunodeficiency virus (SIV).

-!- SUBUNIT: Self-associates. Also heterodimer of MIP-1-alpha(4-69) and MIP-1-beta(3-69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: N-terminal processed form LD78-alpha(4-69) is produced by proteolytic cleavage after secretion from HTLV1-transformed T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted.
INDUCTION: By TPA or PHA (TPA = 12-o-tetradecanoyl phorbol-13
acetate (tumor promoter); PHA = phytohemagglutinin (T-cell
                                                                                             STRUCTURE OF 24-92 BY NMR, AND MUTAGENESIS OF ASP-49 AND GLU-89.
PubMed=12401480; DOI=10.1016/S1359-6101(02)00045-X; Menten P., Wuyts A., Van Damme J.; "Macrophage inflammatory protein-1.";
                                                       Cytokine Growth Factor Rev. 13:455-481(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000827; CC chemkine sml.
InterPro; IPR01811; Chemokine_ILB.
Pfam; PF00048; ILB; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M25315; AAA57255.1; -.
EMBL; X03754; CAA27388.1; -.
EMBL; X04018; CAA27643.1; ALT_SEQ.
EMBL; M23178; AAA35858.1; -.
EMBL; D90144; BAA14172.1; -.
EMBL; AF043339; AAC03539.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; AF043339; AAC03539.1; -. A35673; A30574.
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PDB; 1B53; NNR; A/B=24-92.
Genew; HGNC:10627; CCT:7
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SY04 CHICK STANDARD; PRT; 90 AA.
090826; Q910C9;
01.NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Small inducible cytokine A4 homolog precursor (Macrophage inflammatory protein 1-beta homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95369710; PubMed=7642115; DOI=10.1016/0378-1119(95)00210-W; Petrenko O., Ischenko I., Enrietto P.J.; Petrention of a cDNA encoding a novel chicken chemokine homologous to mammalian macrophage inflammatory protein-1 beta."; Gene 160:305-306(1995).
                                                                                                                                                                                                                                                                                                                                     1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                            2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perrenko O., Enrietto P.J.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Monokine with inflammatory and chemokinetic properties
                                                                                           BB-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20049023; PubMed=10582310;
Hughes S., Bumstead N.;
"Mapping of the gene encoding a chicken homologue of the mammalian
                                                                                           ij
Chemotaxis; Cytokine; Direct protein sequencing
                                                                                         D->A: Reduces self-association;
10010: Improved pharmaceutical
                                                                                                                                  E->A: Reduces self-association.
                                                                                                                                                                                                                                                                                Length 92;
                                                                                                                                                                                                                                                                               46.8%; Score 236; DB 1; Length 92 48.4%; Pred. No. 4.5e-19; ive 22; Mismatches 23; Indels
                                       cytokine A3
                                                                                                                                                                                                                                                        10085 MW; 517865D5D6776CA8 CRC64;
                                     Small inducible cyl
MIP-1-alpha(4-69).
                                                             By similarity.
By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                           61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMK 91
                                                                                                                                                                                                                                                                                                                                                                                                          properties
              response; Signal.
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SEQUENCE OF 14-90 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=CCL4; Synonyms=SCYA4;
                                                                                                                                                                                                                                                                                                            44; Conservative
                          23
92
92
73
49
                                                                                                                                    (By similarity).
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Best Local Similarity
Matches 44; Conserv
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                                                                                                                                                                                                                                                        92 AA;
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                                     433
434
49
                                                                                                                                    Inflammatory
                                                               DISULFID
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                                                                                           MUTAGEN
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                          SIGNAL
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MOUSE
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                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   By similarity.
Small inducible cytokine A4 homolog.
By similarity.
By similarity.
M -> L (in Ref. 1).
50AF9679A267408F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hughes S.M., Bumstead N.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, PH146739, AAD48772.1;
GO, GO:0005576; C:extracellular; IEA.
GO, GO:0008009; F:chemokine activity; IEA.
GO, GO:0008095; P:mmune response; IEA.
InterPro; IPR000827; CC.chemkine sml.
InterPro; IPR001811; Chemokine_IE8.
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SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 90 AA; 9986 MW; 50AF9679A2675ICB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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17; Mismatches
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PROSITE; PS00472; SMALL CYTOKINES CC; 1.
Chemotaxis; Cytokine; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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HSSP; P12316; 1HUM.
INTERPRO; IPRO00827; CC Chemkine sm
InterPro; IPR001811; Chemokine_IE8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9987 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity 47.3
44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
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1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS 60

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1 MKVSVAALAVLL---IAICYQTSAAPVGSDPPTSCCFTYISRQLPFSFVADYYETNSQCP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89993958; PubMed-2521353; Brown K.D., Zurawski G.; Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.; Memall inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence polymorphisms in the chemokines Scyal (TCA-3), Scya2 (monocyte chemoattractant protein (MCP)-1), and Scyal2 (MCP-5) are candidates for eas7, a locus controlling susceptibility to monophasic remitting/nonrelapsing experimental allergic encephalomyelitis.";
J. Immunol. 163:2262-2266(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: Monokine with inflammatory and chemokinetic properties.
-1- SUBUNIT: Homodiner (By similarity).
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                        (Macrophage inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sherry B., Tekamp-Olson P., Gallegos C., Bauer D., Davatelis G., Wolpe S.D., Masiarz F., Coit D., Cerami A.; "Resolution of the two components of macrophage inflammatory protein 1, and cloning and characterization of one of those components, macrophage inflammatory protein 1 beta."; J. Exp. Med. 168:2251-2259(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=B10.S/J, and SJL/J; TISSUE=Spleen;
BIDLINES=93730037; PubMed=10438970;
Tenscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
Blankenhorn E.P.;
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                  01-07N-1990 (Rel. 13, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Small inducible cytchine A4 precursor (CCL4) (Macrophage inflamm protein 1-beta) (MIP-1-beta) (H400 protein) (SIS-gamma) (ACT2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=DBA/2J; TISSUB=Liver;
Daubersies P., Lepretre F., Bailleul B., Grove M., Pragnell I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plumb M.A.;
Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
                                                                 |:||||::| || || || || HAGVVFITRKGREVCANPQNDWVQDYMNKMELN 90
                                           61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
                                                                                                                                                                                              92 AA.
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                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                               Name=Cc14; Synonyms=Miplb, Scya4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89067830; PubMed=3058856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activation processes."; J. Immunol. 142:679-687(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M23503; AAA40148.1; -.
EMBL; M35590; AAA39708.1; -.
EMBL; X62502; CAA44364.1; -.
EMBL; AF128218; AAF22559.1; -
                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Gaps

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Indels

A4

9 59

CHAIN

Matches

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                                                                                                                                                                                                                              1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
                                                                                                                                                                                                                                                  1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYETNSQCS
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01-OCT-1996 (Rel. 34, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Small inducible cytokine Ap precursor (CCL4) (Macrophage inflammatory protein 1-beta) (MIP-1-beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, InterPro, InterPro, InterPro, InterPro, InterPro, IPR001811, I.B. R. Pfan, PR00418; IL8; IL. SWART; SM00199; SCT; I. DR. PROSITE; PS00472; SMALL_CYTOKINES_CC; I. DR. PROSITE; PS00472; SMALL_CYTOKINES_CC; I. DR. PROSITE; PS00472; SMALL_CYTOKINES, Signal.

FT SIGNAL 1 23 SM1 inducible cytokine A4. PT CHAIN 24 SM1 inducible cytokine A4. PT CHAIN 34 58 By similarity.

TRULFID 34 58 By similarity.

35 74 MW; 60B45IEEEBG7103D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.5%; Score 229.5; DB 1; Length 92; 44.1%; Pred. No. 2.5e-18;
                                                                                                                                            DB 1; Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.1%; Pred. No. 4.55-10,
                 By similarity.
Small inducible cytokine
                                                                                                 ECBA8818D42A735C CRC64;
Inflammatory response; Signal.
                                                                                                                                                                                     32;
                                                                                                                                          45.7%; Score 230.5; DB 1
45.2%; Pred. No. 1.9e-18;
                                                                                                                                                                                                                                                                                                                                      60 QPAVVFQTKKGRQVCANPSESWVQEYVDDLELN 92
                                                                                                                                                                                                                                                                                                              61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
                                                                                                                                                                                     18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 AA.
                                                        By similarity. By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Cc14; Synonyms=Mip1b, Scya4;
Rattus norvegicus (Rat)
                                                                                                 10066 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U06434; AAA96497.1; -. HSSP; P13236; 1HUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 44.1
Matches 41; Conservative
                                                                                                                                                                                     42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                       23
74
74
Chemotaxis; Cytokine;
                                                                                                                                                             Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                 92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SY04 RAT
P50230;
                                                            DISULFID
                                                                               DISULFID
                                                                                                   SEQUENCE
                                                                                                                                              Query Match
                     SIGNAL
                                         CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 44, Last annotation update)
Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory
protein 1-beta) (MIP-1-beta) (Immune activation protein 2) (ACT-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=New Zealand white;
MEDLINE=84198239; PubMed=8148323;
MEDLINE=9419829; PubMed=8148323;
Mori S., Goto K., Goto F., Mutakami K., Ohkawara S., Yoshinaga M.;
"Dynamic changes in mRNA expression of neutrophils during the course of acute inflammation in rabbits.";
Int. Immunol. 6:149-156(1994).
Int. Immunol. 6:149-156(1994).
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=CCL4; Synonyms=SCYA4;
Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                  46.5%; Score 234.5; DB 1; Length 92;
45.2%; Pred. No. 6.7e-19;
tive 20; Mismatches 30; Indels
                                                                                                                                                                                                                              Small inducible cytokine A4
                                                                                                                                                                                                                                                  By similarity.
By similarity.
8853FD58FDE61BAC CRC64;
               PIR; C30552; C30552.
HSSP; P13254; JHUM.
MGD; MGI: 98261; CC14.
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_ILB.
Ffam; PR00189; SCY; 1.
SMART; SM00199; SCY; 1.
PR05ITE; PS00472; SMALL, CYTOKINES_CC; 1.
CHEMOCIAXis; Cytokine; Inflammatory response; Signal.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 KPAVVFLTKRGRQICANPSEPWVTEYMSDLELN 92
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InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_ILB.
Pfam; PF00048; ILB; L.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                                                                                                                                         92 AA; 10168 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D17402; BAA04226.1; -. PIR; 146730; 146730.
EMBL; AF128219; AAF22560.1;
                                                                                                                                                                                                                                                                                                                                                       Local Similarity 45.2
nes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (By similarity).
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ID SY04 RABIT
                                                                                                                                                                                                                                                                     DISULFID
SEQUENCE
                                                                                                                                                                                                                                                  DISULFID
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1; Gaps

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SEQUENCE FROM N.A.
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SO OS SE DE LA CONTRA LA C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDILINE_22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;
Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
"Molecular cloning and sequencing of 25 different rhesus macaque chemokine cDNAs reveals evolutionary conservation among C, CC, CXC, AND CX3C families of chemokines.";
Cytokine 18:140-148(2002).
EMBL; AR749267; AAN76071.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Home sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 45.5%; Score 229.5; DB 2; Length I Similarity 44.1%; Pred. No. 2.5e-18; 41; Conservative 20; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nibbs R.J., Barcellos L.F., Townson J.R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AX079147; AAL87008.1; -.
PIR; C60407; C60407.
HSSP; P13236; 1HVM.
GO; GO:0005576; C:extracellular; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00048; ILB; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 92 AA; 10103 WW; 8082C2071565F809 CRC64;
                                                                                                                                                                                                                                                                                                                                       01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chemokine CCL4/WIP-1BETA.
Macaca mulatta (Rhesus macaque).
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Macrophage inflammatory protein-1b2.
                                                                        60 QPAVVFLTKKGRQICADPSEPWVNEYVNDLELN 92
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                                61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR000827; CC chemkine sml.
InterPro; IPR001811; Chemokine_IEa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
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08HYO2
AC Q8HYQ2
AC Q8HYQ2
DT 01-MA
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08NHW
AC 08NHW
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AC 08NHW
DT 01-0C
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DE MACIO
GN NAME
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RRP SEQUE
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191336, P22617; Q13704;

101-JAN-1990 (Rel. 13, Created)

101-JAN-1990 (Rel. 13, Last sequence update)

25-OCT-2004 (Rel. 45, Last annotation update)

Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory protein 1-beta) (MIP-1-beta) (MIP-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 45.3%; Score 228.5; DB 2; Length 92; Best Local Similarity 44.1%; Pred. No. 3.2e-18; Matches 41; Conservative 20; Mismatches 31; Indels
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44.1%; Pred. No. 7.1e-18;
tive 19; Mismatches 32; Indels 1
                                                                                                                                                                                                          Pfam; PF00048; IL8; 1. SMART; SM00199; SCY; 1. SMART; SM00499; SCY; 1. SK00472; SK00472; SKMLL CYTOKINES CC; 1. SEQUENCE 92 AA; 1016\overline{6} MW; 4C8\overline{b}01E926CDE882 CRC64;
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PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 92 AA; 10197 MW; 7628FBC425BCED9C CRC64;
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Last annotation update)
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GO; GO:0008009; F:chemokine activity; GO; 0006955; P:immune response; IER InterPro; IPR000827; CC chemkine sml. InterPro; IPR001811; Chemokine_ILB.
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InterPro; IPR01811; Chemokine_ILB.
Pfam; PF00048; ILB; 1.
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nes 41; Conservative
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EMBL;
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 SEQUENCE FROM N.A. MEDLINE=89093958; PubMed=2521353; MEDLINE=89093958; PubMed=2521353; Brown K.D., Zurawski G.; Afamily of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes."; Jimmunol. 142:679-687(1989).
                                                                                                     MEDLINE-89071764; PubMed=2462251;
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"Identification, cloning, and characterization of an immune activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chang H.C., Reinherz E.L., ^{\prime} "Isolation and characterization of a cDNA encoding a putative cytokine which is induced by stimulation via the CD2 structure on human T
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DO1=10.1002/(SICI)1521-4141(199802)28:02<582::AID-IMMU582>3.3.CO;2-1;
Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G.,
Meise M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The gene encoding the Act-2 cytokine. Genomic structure, HTLV-I/Tax
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=91061800; PubMed=2247088; DOI=10.1016/0161-5890(90)90097-J;
MEDLINE=91061800; PubMed=2247088; DOI=10.1016/0161-5890(90)90097-J;
Baixeras E., Roman-Roman S., Jitsukawa S., Genevee C., Mechiche S.,
Vieggas-Pequignot E., Hercend T., Triebel F.;
"Cloning and expression of a lymphocyte activation gene (LAG-1).";
Mol. Immunol. 27:1091-1102(1990).
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Zipfed P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.;
"Mitogenic activation of human T cells induces two closely related
genes which share structural similarities with a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=91373378; PubMed=1894635;
Napolitano M., Modi W.S., Cevario S.J., Gnarra J.R., Seuanez H.N.,
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 6-92 FROM N.A.
BEDLINES-80038522; PubMed-2809212;
Miller M.D., Hata S., Waal Malefyt R., Krangel M.S.;
"A novel polypeptide secreted by activated human T lymphocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Birren B., Fasman K., McKernan K., Nusbaum C., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       responsiveness of 5' upstream sequences, and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lander E.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 85:9704-9708 (1988)
            Name=CCL4; Synonyms=LAG1, MIP1B, SCYA4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      localization.";
J. Biol. Chem. 266:17531-17536(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Immunol. 19:1045-1051(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89325421; PubMed=2568930;
                                                                                                                                                                                                                                                               J. Immunol. 142:1582-1590(1989)
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[Contains: MIP-1-beta(3-69)]
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                           (Human)
                                                                                                                                                                                                                                                    secreted factors.";
                                                                                        SEQUENCE FROM N.A.
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                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphocytes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leonard W.J.;
                           Homo sapiens
                                                                                                                                               gene."
BARXXBBLTAXBBLAXBBLAXBBLTTTAAXXBBLTTAAXBBLTABAXBBLTTTTABAXBBLTTTTABAXBBLTTTTAAXBBLTTTAAXBBCTTTTAAXBBCTABAXBBCT
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                                                                                                                                                                                                                                                                                                             IDENTIFICATION OF MIP-1-BETA(3-69) BY MASS SPECTROMETRY, FUNCTION, AND
                                                                                                                                                                                                                                                                                                                                                           PubMed=12070155; DOI=10.1074/jbc.M203077200;
Guan E., Wang J., Roderiquez G., Norcross M.A.;
"Natural truncation of the chemokine MIP-1beta /CCL4 affects receptor pecificity but not anti-HIV-1 activity.";
J. Biol. Chem. 277:32348-32352(2002).
"Identification of the CC chemokines TARC and macrophage inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             jymphocytes.
-!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                  protein-1 beta as novel functional ligands for the CCRB receptor.";
Eur. J. Immunol. 28:582-588(1998).
                                                                                                                                                                                             "Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major HIV-suppressive factors produced by CD8+ T cells."; Science 270:1811-1815(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             beta(3-69).
-!- SUBCELLULAR LOCATION: Secreted.
-!- INDUCTION: By mitogens.
-!- PTM: N-terminal processed form MIP-1-beta(3-69) is produced by proteolytic cleavage after secretion from peripheral blood
                                                                                                                                                       Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=12401480; DOI=10.1016/S1359-6101(02)00045-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine Growth Factor Rev. 13:455-481 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Menten P., Wuyts A., Van Damme J.;
"Macrophage inflammatory protein-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA51576.1; -.
CAA37723.1; -.
CAA37722.2; ALT_SEQ.
                                                                                                                       MEDLINE=96106406; PubMed=8525373;
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EMBL; M25316; AAA57256.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JH0319; A31767.
PDB; 1HUM; NMR; A/B=24-92.
PDB; 1HUN; NMR; A/B=24-92.
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X53682;
                                                                                                       FUNCTION
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Wagner L., Shamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., TOSHIYUKI S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
Maring M., Marra M.A.;
Jones S.J., Marra M.A.;
Maring M., Andar A., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.;
Manda M., Schmutz J., Myers R.M., Schein J.E.,
Jones S.J., Marra M.A.;
Manda M., Schmutz J., Myers R.M., Schein J.E.,
Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLCVTVLSLLVLVA-AFCSLALSAPMGSDPPTACCFSYTARKLPHNFVVDYYETSSLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYON MOUSE STANDARD; PRT; 92 AA.
P10855; P14096;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1980 (Rel. 14, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory protein 1-alpha) (MIP-1-alpha) (TY-5) (SIS-alpha) (Heparin-binding chemotaxis protein) (L2025).
Name=CCl3; Synonyms=Mipla, Scya3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=88258380; PubMed=3290382;
Davatelis G., Tekamp-Olson P., Wolpe S.D., Hermsen K., Luedke C.,
Gallegos C., Coit D., Merryweather J., Cerami A.;
"Cloning and characterization of a cDNA for murine macrophage
"Cloning and characterization of a novel monokine with inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 44.3%; Score 223.5; DB 2; Length 92; Best Local Similarity 43.0%; Pred. No. 1.2e-17; Matches 40; Conservative 20; Mismatches 32; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC070310; AAH70310.1; -.
HSSP; P10147; 1B50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 92 AA; 10147 MW; 6A567D8926CDE89F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO, GO:0005576; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR000827; CC_chemkine sml.
InterPro; IPR001811; Chemokine_ILB.
Pfam; PF00048; ILB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. TISSUE=Pooled;
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                                                               R GO; GO:0005615; C:extracellular space; TAS.
R GO; GO:0005615; C:extracellular space; TAS.
R GO; GO:0008009; F:chemokine activity; TAS.
GO; GO:000115; P:cell adheaton; TAS.
R GO; GO:000115; P:cell adheaton; TAS.
R GO; GO:000151; P:cell growth and/or maintenance; TAS.
R GO; GO:0001527; P:cell growth and/or maintenance; TAS.
R GO; GO:000153; P:cell signaling; TAS.
R GO; GO:000555; P:immune response; TAS.
R GO; GO:000555; P:immune response; TAS.
R GO; GO:000555; P:immune response; TAS.
R GO; GO:001655; P:immune response; TAS.
R GO; GO:001655; P:immune response; TAS.
R GO; GO:001655; P:immune response; TAS.
R GO; GO:001657; P:inflamatory response; TAS.
R GO; GO:001657; P:inflamatory response; TAS.
R GO; GO:0010975; P:viral genome replication; TAS.
R InterPro; IPR000827; CC_chemkine_sml.
R InterPro; IPR001811; Chemokine_IE8.
R SMART; SM00199; SCY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   SMART, SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
3D-structure; Chemotaxis; Cytokine; Inflammatory response; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.5%; Score 224.5; DB 1; Length 92; 43.0%; Pred. No. 9.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Small inducible cytokine A4.

MIP-1-beta(3.69).

By similarity.

T -> C (in Ref. 7).

A -> S (in Ref. 6).

P -- L (in Ref. 2).

ARKLPR -> REASS (in Ref. 3).

S -> I (in Ref. 8).

S -> G (in Ref. 6).

S -> G (in Ref. 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.0%; Pred. No. y.Je-rv,
rive 20; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10212 MW; F2EA7CF341B0E258 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Name-CCLII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 QPAVVFQTKRSKQVCADPSESWVQEYVYDLELN 92
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115
120
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133
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159
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Pooled;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
DISULFID
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Matches

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06088
AC 06088
AC 06088
DT 05-JU
DT 05-JU
DT 05-JU
DE Chemo
CR HOMO
OC BUKAR
OC BUKAR
OC MAMMA
OC NCBI
RN | [1]
RN | [1]
RN | [1]
RN | [1]

9 29

1; Gaps

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1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYBTNSQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Small inducible cytokine A3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
By similarity.
F -> L (in Ref. 3).
V -> A (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE, PS00472; SMALL CYTOKINES_CC; 1.
Chemotaxis, Cytokine; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.2%; Score 223; DB 1; 45.2%; Pred. No. 1.4e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:98260; Ccl3.
GO; GO:0008009; F:chemokine activity; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000827; CC_chemkine_sml
InterPro; IPR001811; Chemokine_ILB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                            "X5372; CAA31047.1; ...
"X5372; CAA31047.1; ...
"X5372; CAA31047.1; ...
"J04491; AAA40304.1; ...
"MAT061; AAA40307.1; ...
"AF065940; AAC17508.1; ...
"AF065942; AAC17508.1; ...
"AF065942; AAC17508.1; ...
"AF065943; AAC17508.1; ...
"AF065943; AAC17508.1; ...
"AF065943; AAC17508.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inflammatory response; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10345 MW;
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nes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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23
52
62
62
63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00048; IL8; 1.
                                                                                                                                                                                                                                                                                                                                                                                   PIR; S11685; A32393.
HSSP; P10147; 1B50.
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62 2 3 3 4 4
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CONFLICT
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P50229;
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                                EMBL;
EMBL;
EMBL;
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EMBL;
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EMBL;
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J. Exp. Med. 167:570-581(1988).
Properties. Mas a potent chemotactic activity for ecsinophils. Binding to a high-affinity receptor activates calcium release in
                                                                                                                                                                                                                                                                                                   MEDLINE=89993958; PubMed=2521353; MEDWAN T.R., Zurawski G.; Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.; Memall inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence polymorphisms in the chemokines Scyal (TCA-3), Scya2 (monocyte chemoattractant protein (MCP)-1), and Scyal2 (MCP-5) are candidates for eac?, a locus controlling susceptibility to monophasic remitting/nonrelapsing experimental allergic encephalomyelitis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed in lung, spleen, and pancreas.
-!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic structure of murine macrophage inflammatory protein-1 alpha and conservation of potential regulatory sequences with a human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grove M., Lowe S., Graham G., Pragnell I., Plumb M.;
Sequence of the murine haemopoietic stem cell inhibitor/macrophage
inflammatory modesin 1 alpha gene ".
                                                                                                                                     Davatelis G., Tekamp-Olson P., Wolpe S.D., Hermsen K., Luedke C., Gallegos C., Coit D., Merryweather J., Cerami A.;
J. Exp. Med. 170:2189-2189(1989).
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MEDLINE-91237116; PubMed-2033269;
Widmer U., Yang Z., van Deventer S., Manogue K.R., Sherry B.,
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Kwon B.S., Weissena S.M.;
"cDN sequency sequences";
"cDN sequency Sci. U.S.A. 86:1963-1967(1989)
proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory protein 1 alpha gene.";
Nucleic Acids Res. 18:5561-5561(1990)
chemokinetic properties.";
J. Exp. Med. 167:1939-1944(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activation processes.";
J. Immunol. 142:679-687(1989).
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                                                                                                        REVISIONS.
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7 9 28

Gaps

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Length 92;

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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
55-JUL-2004 (Rel. 44, Last annotation update)
55mall inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory protein 1-alpha) (MIP-1-alpha).
                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                        TISSUE=Lung;
MEDLINE=95298037; PubMed=7779098;
Shi M.M., Godleski J.J., Paulauskis J.D.;
"Molecular cloning and posttranscriptional regulation of macrophage inflammatory protein-1 alpha in alveolar macrophages.";
Biochem. Biophys. Res. Commun. 211:289-295(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Long Evans; TISSUE=Lung; MEDLINE=95238990; PubMed=7722328; Shanley T.P., Schmal H., Friedl H.P., Jones M.L., Ward P.A.; Shanley T.P., Schmal H., Friedl H.P., Jones M.L., Ward P.A.; Role of macrophage inflammatory protein-1 alpha (MIP-1 alpha) in acute lung injury in rats."; J. Immunol. 154:4793-4802(1995).
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Sigmodon.
NCBI_TaxID=42415;
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                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
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                     MEDLINE=96183056; PubMed=8607872; DOI=10.1006/bbrc.1996.0511;
Nakagawa H., Shiota S., Takano K., Shibata F., Kato H.;
Nakagawa H., Shiota S., Takano K., Shibata F., Kato H.;
"Cytokine-induced neutrophil chemoattractant (CINC)-2 alpha, a novel
member of rat GRO/CINCs, is a predominant chemokine produced by
lipopolysaccharide-stimulated rat macrophages in culture.";
Biochem. Biophys. Res. Commun. 220:945-948(1996).
-- FUNCTION: Monokine with inflammatory and chemokinetic properties.
Has chemotactic activity for monocytes, neutrophils, eosinophils,
basophils, and lymphocytes. Required for lung fNr-alpha
production, neutrophil recruitment and subsequent lung injury and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
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                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Secreted.
INDUCTION: By lipopolysaccharide (LPS).
SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
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                                                                                                                                                            may function as an autocrine mediator for the macrophage production of TNF-alpha which in turn up-regulates vascular adhesion molecules required for neutrophil influx. This protein
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00472; SMALL CYTOKINES CC; 1.
Chemotaxis; Cytokine; Direct protein sequencing; Heparin-binding;
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1.4e-17;
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C -> W (in Ref. 2 and 3).
14E861C647F9A2EB CRC64;
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RGD; 3647; CCl3.
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_ILB.
PF000948; ILB; 1.
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01-DEC-2001 (TrEMBLrel. 19, Created)
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Q91ZLAC

Q91ZLDDT

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DT Name=

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GS Sigmo

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SEQUENCE FROM N.A.
MEDLINE-22079879; PubMed=12085325;
Blanco J.C., Richardson J.Y., Darnell M.E., Rowzee A., Pletneva L.,
Porter D.D., Prince G.A.;
"Cytokine and chemokine gene expression after primary and secondary
respiratory syncytial virus infection in cotton rats.";
J. Infect. Dis. 185:1780-1785(2002).
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Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
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Last sequence update)
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41.9%; Pred. No. 1.6e-17;
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KPAVVFLTRKGKEVCADPSQPWVNEYVNDLELN
                                                                                                                                                                                                                                                                                                                                                                                  chemokines, and interferons.";
U. Interferon Cytokine Res. 24:21-28(2004)
EMBL; AF421392; AALL6933.1; -.
HSSP; P13236; 1HUM.
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GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
Pfam; PF00048; ILB; 1.
SMART; SM0199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR001827; CC chemkine sml.
InterPro; IPR001811; Chemokine_IE8.
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8857 MW;
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Matches 38; Conservative
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16
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SMART; SM00199; SCY; 1.
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SEQÜENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKVPGAALA-VLLCTMSLCSQV-FSPFGADTPIACCFSYVSKQIPRKFIVDCFETSSQCS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schountz T., Buniger A., Davenport B., Hegg T.; "Cloning of deer mouse IL-2, IL-12 p35, IL-21, GM-CSF, CCL3 and CCL4
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ishizuka K., Igata-Yi R., Naruse K., Nakashima H., Ohuchi K.,
Katsuragi S., Kin Y., Ohmoto Y., Nomiyama H., Ilo M., Miura R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.2%; Score 217.5; DB 2; Length 85; 45.3%; Pred. No. 5.4e-17; ive 17; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miyakawa T.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNAB.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 AA; 9345 MW; B87216EB9B41F34C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR000827; CC_chemkine sml.
InterPro; IPR001811; Chemokine_IE8.
Ffam, PF00048; IE8, 1.
FMANT; SW00199; SCY; 1.
PROSITE; PS00472; SWALL_CYTOKINES_CC; 1.
                                                                                                                                                                                                             85 AA
                                                                       61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KPGIVFITKRGHSVCTNPSDKWVQDY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | : | | : | | : | | : | | : | XPAVVFLTRKGKQVCADPSLPWVNEY 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LD78 alpha beta precursor (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                        Peromyscus maniculatus (Deer mouse)
                                                                                                                                                                                                                                                                                                                           chemokine ligand 4 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY247758; AAP04417.1; -.
HSSP; P13236; 1HUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D63785; BAA09855.1; -.
                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 45.39
hes 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                             PRELIMINARY;
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TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Peromyscus.
                                                                                                                                                                                                                                                                                                                           CC chemokin
Name=Cc14;
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                                                                                                                                                                                                             080XG5
                                                                                                                                                        RESULT 22
080XGS
1D Q80XG
AC Q80XG
AC Q80XG
DT O1-JT
DT O1-JT
DT O1-JT
DT O1-GC
CI
GN Name
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014745
AC 01474
DT 01-NO
DT 01-NO
DT 01-NO
DT 01-NO
DT 01-NO
DE LD78
OS BUAMO
OC MAMMO
OX NOEL
RR SEQUE
RR ITISSU
RA KATSU
RA KATSU
RA KATSU
RA KATSU
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EMBL, AR457195; AANT6985.1; ...
                                                                                                                                                                                                                                                                                                                                               12 LLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYETNSQCSKPGIVFITKRG
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                DB 2; Length 80;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                       8B509EB15648E971 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 AA; 6442 MW; EB12A0E0D41D6F68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Macrophage inflammatory protein 1 alpha (Fragment)
Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                             42.4%; Score 213.5; DB 2;
50.0%; Pred. No. 1.5e-16;
tive 18; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.5%; Score 209; DB 2;
llarity 57.1%; Pred. No. 3.3e-16;
Conservative 14; Mismatches 10.
                                                                                                                 LD78 alpha beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR000827; CC chemkine sml.
InterPro; IPR001811; Chemokine_IE8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PP00048; ILB; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1
                                                                                      Potential
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Figdor
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RAHARA KARAKA KA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    associated CC chemokine 1) (AMAC-1) (Dendritic cell chemokine 1) (DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Small inducible cytokine Al8 precursor (CCL18) (Macrophage inflammatory protein 4) (MIP-4) (Pulmonary and activation-regulated chemokine) (CC chemokine PARC) (Alternative macrophage activation-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20170941; PubMed=10704244; DOI=10.1006/cyto.1999.0543; Sick C., Schneider K., Staeheli P., Weining K.C.; "Novel chicken CXC and CC chemokines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=CCL18; Synonyms=AMAC1, DCCK1, MIP4, PARC, SCYA18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chemokine K203.
6FA2EA7A4950CA75 CRC64;
                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.5%; Score 209; DB 2;
43.0%; Pred. No. 5.3e-16;
tive 18; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Macrophage inflammatory protein-3 and -4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytokine 12:181-186 (2000)

EMBL; Y18692; CAB70956.1; -.

HSSP; Q16663; 2HCC.

GO; GO:0005976; C:extracellular; IEA.

GO; GO:0006959; P:chemokine activity; IEA.

GO; GO:0006959; P:chemokine response; IEA.

InterPro; IPR001811; Chemokine_ILB.

PFam; PP00048; ILB; 1.
                                                                         83
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TISSUE=Aorta, and Lung;
MEDLINE=971376836; PubMed=9233607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential.
                                                                                                                            Created)
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                                                                                                                                                     (TrEMBLrel. 15, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 AA; 9896 MW;
                                                                                                                          (TrEMBLrel. 15,
                                                                                                                                                                                                      Chemokine K203 precursor.
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                                                                         PRELIMINARY;
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89
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40; Conserv
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                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                       01-OCT-2000 (
01-OCT-2000 (
01-JUN-2003 (
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                                                                                                                                                                                                                                    Name=K203;
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                                                                         Q918E0
                                                                                                                                                                                                                                                                                                                                           Gallus
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ID SY18 HUMAN

DT 01-NOV.

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SEQUENCE FROM N.A.

Politz O., Kodelja V., Guillot P., Orfanos C.E., Goerdt S.;
Politz O., Kodelja V., Guillot P., Orfanos C.E., Goerdt S.;
Politz O., Kodelja V., Guillot P., Orfanos C.E., Goerdt S.;
Within the first intron sequence.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Chemctactic factor that attracts lymphocytes but not monocytes or granulocytes. May be involved in B cell migration into B cell follicles in lymph nodes. Attracts naive T lymphocytes toward dendritic cells and activated macrophages in lymph nodes, has chemctactic activity for naive T cells, CD4+ and CD8+ T cells and thus may play a role in both humoral and cell-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunity responses.
SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: Expressed at high levels in lung, lymph nodes, placents, bone marrow, dendritic cells present in germinal centers and T-cell areas of secondary lymphoid organs and macrophages derived from peripheral blood monocytes. Not expressed by peripheral blood monocytes and a monocyte-to-macrophage differentiation is a prerequisite for expression.
INDUCTION: Specifically induced in macrophages by IL-4, IL-13, and IL-10. Expression is inhibited by IR-9 glucocorticoids exert a slightly positive synergistic effect in combination with IL-4. Strongly induced in several human cell lines, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97275308; PubMed=9129202;
Wells T.N.C., Peitsch M.C.;
"The chemokine information source: identification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99168908; PubMed=10049593; DOI=10.1006/geno.1998.5670; Tasaki Y., Fukuda S., Iio M., Miura R., Imai T., Sugano S., Yoshie O., Hughes A.L., Nomiyama H.; "Chemokine PAKC gene (SCYA18) generated by fusion of two MIP-Ialpha/LD78alpha-like genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kodelja V., Mueller C., Politz O., Hakij N., Orfanos C.E., Goerdt S., "Alternative macrophage activation-associated CC-chemokine-1, a novel structural homologue of macrophage inflammatory protein-1 alpha with a Th2-associated expression pattern."; Inflammatory protein-1 alpha with J. Immunol. 160:1411-1418(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    novel chemokines using the WorldWideWeb and expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'A dendritic-cell-derived C-C chemokine that preferentially attracts
Hieshima K., Imai T., Baba M., Shoudai K., Ishizuka K., Nakagawa T. Tsuruta J., Takeya M., Sakaki Y., Takatauki K., Miura R., Opdenakker G., van Damme J., Yoshie O., Nomiyama H.; "A novel human CC chemokine PARC that is most homologous to macrophage-inflammatory protein-1 alpha/LD78 alpha and chemotactic T. lymphocytes, but not for monocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=99189237; PubMed=10087196; DOI=10.1006/geno.1998.5635;
Guan P., Burghes A.H.M., Cunningham A., Lira P., Brissette W.H.,
Neote K., McColl S.R.;
"Genomic organization and biological characterization of the novel
human CC chemokine DC-CK-1/PARC/MIP-4/SCYA18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adema G.J., Hartgers F., Verstraten R., de Vries E., Marland G., Menon S., Foster J., Xu Y., Nooyen P., McClanahan T., Bacon K.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Dendritic cell;
MEDLINE=97336102; PubMed=9192897; DOI=10.1038/42716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leukoc. Biol. 61:545-550(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98230488; PubMed=9570561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 387:713-717(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISCUSSION OF SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     naive T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     databases."
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EMBL; U85767; AAB51134.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         databases."
                                                                                                                                                                                                                                                                         receptor
MM; 603757; -...

R GO; GO:0008009; F:chemokine activity; TAS.

R GO; GO:0008009; F:chemokine activity; TAS.

R GO; GO:0019715; P:antimicrobial humoral response (sensu Verte. . .; TAS.)

R GO; GO:00018715; P:cell.-cell signaling; TAS.

R GO; GO:0006955; P:chemotaxis; TAS.

R GO; GO:0006955; P:cesponse to biodic stimulus; TAS.

R GO; GO:0006955; P:response to biodic stimulus; TAS.

R GO; GO:0006955; P:signal transduction; TAS.

R GO; GO:000165; P:signal transduction; TAS.

R TherPro; IPR00247; C-X-C/InterlArn 8.

InterPro; IPR001811; Chemokine_ID8.

InterPro; IPR001811; Chemokine_ID8.

R Ffan; PF00048; ID8; I.

RRINTS; PR00448; ID8; INTERLEWINNS.

R PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LAAALLVLVCTMALCSCAQVGTNKEL-----CCLVYTSWQIPQKFIVDYSETSPQ 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SY23_HUMAN STANDARD, PRT; 120 AA.
PS5773_3 (000174; 075950;
01-N0V-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
8mall inducible cytokine A23 precursor (CCL23) (Macrophage inflammatory protein 3) (MIP-3) (Myeloid progenitor inhibitory factor-1) (CK-beta-8) (CKB-8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 VAAIPFFLLITIAL-----GTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYETNSQ
       SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
by phorbol myristate acetate (PMA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     k; Score 208; DB 1; Length 89;
k; Pred. No. 6.9e-16;
17; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Small inducible cytokine A18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By similarity.
By similarity.
C287B94B9C0518E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 CPKPGVILLTKRGRQICADPNKKWVQKYISDLKIN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSKPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=CCL23; Synonyms=MIP3, MPIF1, SCYA23;
                                                                                                                                           EMBL; AB012113; BAA34368.1; -... EMBL; AB012113; BAA34368.1; -.. EMBL; AF082214; AAC32287.1; -.. EMBL; AF082213; AAC32287.1; JOINED. EMBL; AF111198; AAD30390.1; -.. HSSP; P10147; 1B50.
                                                                                                                                EMBL; AB000221; BAA21670.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Inflammatory response; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.3%;
42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 AA; 9849 MW;
cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
70
70
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U937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97275308; PubMed=9129202; Wells T.N.C., Peitsch M.C.; "The chemic information source: identification and characterization "The chemic information source: identification of novel chemokines using the WorldWideWeb and expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Youn B.-S., Zhang S.M., Broxmeyer H.E., Cooper S., Antol K., Fraser M. Jr., Kwon B.-S.,

"Characterization of CKDeta8 and CKDeta8-1: two alternatively spliced forms of human beta-chemokine, chemoattractants for neurrophile, monocytes, and lymphocytes, and potent agonists at CC chemokine recentor 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name-Short; Synonyme-CKB-8; Isolablayed; Name-Lord; Synonyme-CKB-8; Isola=P55773-1; Sequence=Displayed; Name-Lord; Synonyme-CKB-8-1; Name-Lord; Synonyme-CKB-8-1; Isola=P55773-2; Squence=V8P 001063; Isola=P55773-2; Squence=V8P 001063; muscle and pancreas. Moderate levels in fetal liver, skeletal marrow and placenta. The short form is the major species and the longer form was detected only in very low abundancy.
-: SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99228475; PubMed=10213461; DOI=10.1089/10799909314153; Nomiyama H., Fukuda S., Iio M., Tanase S., Miura R., Yoshie O.; Nomiyama the chemokine gene cluster on human chromosome 17q11.2 containing the genes for CC chemokine MPIF-1, HCC-2, LEC, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21265011; PubMed=11060285; DOI=10.1074/jbc.M005085200; MEDLINE=21265011; PubMed=11060285; DOI=10.1074/jbc.M005085200; Rajarathnam K., Li Y., Rohrer T., Gentz R.; Solution structure and dynamics of myeloid progenitor inhibitory factor-1 (MPIF-1), a novel monomeric CC chemokine."; J. Biol. Chem. 276:4909-4916(2001).

-!- FUNCTION: Shows chemotactic activity for monocytes, resting T-lymphocytes, shows chemotactic activity for activated lymphocytes. Inhibits proliferation of myeloid progenitor cells in colony formation assays. This protein can bind heparin. Binds CCR1.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                             Patel V.P., Kreider B.L., Li Y., Li H., Leung K., Salcedo T., Nardelli B., Pippalla V., Gentz S., Thotakura R., Parmelee D., Gentz R., Garotte G.; Molecular and functional characterization of two novel human C-C chemokines as inhibitors of two distinct classes of myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interferon Cytokine Res. 19:227-234(1999).
"Macrophage inflammatory protein-3 and -4."; Patent number US5504003, 02-APR-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 22-36.
TISSUE=Aortic endothelium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leukoc. Biol. 61:545-550(1997).
                                                                                                                                                                                                                                          MEDLINE=97258609; PubMed=9104803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Exp. Med. 185:1163-1172(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98226667; PubMed=9558365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lood 91:3118-3126(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Monocytes;
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1 MKVPTAVLAVLACI-ITLCNQVFSAPYGADTPTFCCFSYGR-QIPRKFIADYFQTSSLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYETNSOCS
                                                                                                                     "The cotton rat: an underutilized animal model for human infectious diseases can now be exploited using specific reagents to cytokines, chemokines, and interferons.";
                                                      PubMed=14980081; DOI=10.1089/107999004772719873;
Blanco J.C., Pletneva L., Boukhvalova M., Richardson J.Y.,
Harris K.A., Prince G.A.;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 39.5%; Score 199; DB 2; Length 92; Best Local Similarity 43.0%; Pred. No. 7.6e-15; Matches 40; Conservative 19; Mismatches 32; Indels
                                                                                                                                                                         Juterferon Cytokine Res. 24:21-28 (2004).

EMBL, AX059407, AAL26704.1; --
HSSP, P10147; 1B50.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0006095; F:chemokine activity; IEA.

GO; GO:0006955; P:immune response; IEA.

Pfam; PR00189; ISB; 1.

PROSITE; SM00199; SCY; 1.

PROSITE; SM00172; SMALL CYTOKINES CC; UNKNOWN 1.

SEQUENCE 92 AA; 10334 MW; CF9ĀAB3D94DCAF79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | | : | : | | | | : | : | | | : | | EPGIIFLTKRNRHVCADPKETWVQEIITDLELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00436; INTERLEUKIN8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00048; IL8;
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                                         SEQUENCE FROM N.A
    NCBI_TaxID=42415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=9544;
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  SOR REAL TRANSPORT OF REAL PROPERTY AND REAL PRO
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                                                                                                                                                                                                                          TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Gaps
                                                                                                                                  GO; GO:0008009; F:chemokine activity; TAS.
GO; GO:0008874; P:calcium ion homeostasis; TAS.
GO; GO:0006874; P:call.cell signaling; TAS.
GO; GO:0006915; P:chemotaxis; TAS.
GO; GO:0006955; P:chemotaxis; TAS.
GO; GO:0006955; P:immune response; TAS.
GO; GO:0006955; P:imflammatory response; TAS.
GO; GO:0006957; P:inflammatory response; TAS.
InterPro; IPR00827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_IEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M -> V (in dbSNP:1003645).

/PTId=VAR 011916.

MLVTALGSQĀRVTKDARTEFMASKLPLENPVLL -> HALPLVPGPGHKRCRDRVHECQSFHWKLQYFW (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            091265
01-265;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Macrophage inflammatory protein-1 alpha.
Name=MIP1 alpha;
Sigmodon hispidus (Hispid cotton rat).
Eukaryota, Mecazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                            60 PRSIPCSLLESYFETNSECSKPGVIFLTKKGRRFCANPSDKQVQVCMRMLK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> MLWRRKIGPQMTLSHAAG (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 TYKIPRQRIMDYYETNSQCSKPGIVFITKRGHSVCTNPSDKWVQDYIKDMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.0%; Score 201.5; DB 1; Length 1; 38.7%; Pred. No. 5.2e-15; ive 22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Small inducible cytokine A23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13443 MW; 6CA622DD3A4B27AD CRC64;
                                   EMBL; AF088219; AAC63326.1; -. EMBL; AF088219; AAC63327.1; -. PDB; 1G91; NWR; A=44-120. Genew; HGNC:10622; CCL23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity 38.7 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106
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120 AA;
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Best Local
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1D Q9
AC Q9
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                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875; Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.; "Molecular cloning and sequencing of 25 different rhesus macaque chemokine cDNAs reveals evolutionary conservation among C, CC, CXC, AND CX3C families of chemokines."; Cytokine 18140-148 (2002).

EMBL; AF449272; AAN76076.1; -. HSSP; P10147; 1B50.
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 39.1%; Score 197; DB 2; Length 88; Best Local Similarity 40.4%; Pred. No. 1.2e-14; Matches 40; Conservative 19; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 88 AA; 9797 MW; 19267D02F750D8F CRC64;
                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chemokine CCL18/PARC.
Macaca mulatta (Rhesus macaque).
88 AA.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKISVAAIPFFLLITIALGTKTESSSRGPY - - HPSECCFTYTTYKIPRQRIMDYYETNSQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=LONG Evans; TISSUE=Lung;
Jones M.L., Shanley T.P., Ward P.A.;
Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Chemoattractant for blood monocytes, memory T helper cells and eosinophils. Causes the release of histamine from basophils and activates eosinophils (By similarity).
-!- SUBCELULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Gaps
                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-0UL-2004 (Rel. 44, Last annotation update)
Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES protein) (SIS-delta)
Name=Ccl5; Synonyms=Scya5;
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFam; PF00048; 110, ...
SMART; SM0199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
Chemotaxis; Cytokine; Inflammatory response; Signal; T-cell.
SIGNAL 1 24 Small inducible cytokine A5.
CHAIN 25 92 Small inducible cytokine A5.
DISULFID 34 58 By similarity.
TATULFID 35 74 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

38.6%; Score 194.5; DB 1; Length 92;
Best Local Similarity 42.7%; Pred. No. 2.5e-14;
Matches 38; Conservative 15; Mismatches 31; Indels
                                                      55 TNSQCSKPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
                                                                        92 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 CSKPGIVFITKRGHSVCTNPSDKWVQDYI 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGD; 6969; Ccls.
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR01811; Chemokine_IE8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
                                                                                                                                                                                 PRT;
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                                                                                                                                                                                 STANDARD;
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Search completed: September 19, 2005, 08:57:36 Job time : 177 secs

2005
5:30
12:25
13
Sep
Mon

30 116 23.0 114 31 93 18.5 114 32 86.5 17.2 92 33 85 16.9 101	82 16.3 101 81 16.1 103	77.5 15.4 103 75.5 15.0 103 74 14.7 101		68.5 13.6 311 68.5 13.6 316 67.5 13.4 1379	66.5 13.2 476 66 13.1 942	65.5 13.0 704	64 12.7 114 64 12.7 114	64 12.7 573 63.5 12.6 208 63.5 12.6 461 63 12.5 184	63 12.5 184 63 12.5 184 63 12.5 501 63 12.5 501	62.5 12.4 496	62 12.3 100 62 12.3 100 62 12.3 107 62 12.3 107	62 12.3 182 62 12.3 501 62 12.3 501	71 61.5 12.2 101 72 61.5 12.2 302	74 61.5 12.2 593	61 12.1 104	78 61 12.1 1732	80 60.5 12.0 207	81 60.5 12.0 234 82 60.5 12.0 293	83 60.5 12.0 450 84 60.5 12.0 682	85 60 11.9 113 86 60 11.9 308	87 60 11.9 422	89 59.5 11.8 257	59.5 11.8 257 59.5 11.8 286	92 59.5 11.8 311	94 59.5 11.8 411	95 59.5 11.8 527	97 59.5 11.8 702	chemoattr 99 59.5 11.8 982	Octein prec 100 59 11.7 90 Cottokine	
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Lt.	OM protein - protein search, using sw model	Run on: September 19, 2005, 08:48:11 ; Search ti (without ali; 229.440 Milli	Title: US-10-626-530-2 Perfect score: 504 Sequence: 1 MKISVAAIPPFLLITIALGTVCTNPSDE	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 283416 segs, 96216763 residues	Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries	Database : PIR 79:* 1: pir1:* 2: pir2:*	pir3:	Pred. No. is the number of results predicted by ch score greater than or equal to the score of the re and is derived by analysis of the total score dist	SUMMARIES	Query core Match Leng	240.5 47.7 93 2	2 45.6 46.5 92 2 C30552 4 23.0 4 23.0 5 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	224.5 44.5 92 1	223 44.2 92 2	189 37.5 91 1	180 35.7 116 2	163 32.3 50 2 156 31.0 125 2	153.5 30.5 99 2	150.5 29.9 148 1	149 29.6 148 1 148.5 29.5 99 1	148.5 29.5 99 2	144 28.6 999 2	135.5 26.9 96 2	135.5 26.9 96 2	126 25.0 120 2	123 24.4 96 2 123 24.4 97 2	

lymphotactin precu
TCA3 protein - mou
interleukin-8 - mou
interleukin-8 - mou
interleukin-8 - do
interleukin

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A,Cross-references: UNIPROT:P10147; GB:D90144; NID:g219905; PIDN:BAA14172.1; PID:g219906
R;Zipfel, P.F.; Balke, U.; Irving, S.G.; Kelly, K.; Siebenlist, U.
J. Immunol. 142, 1582-1590, 1999
A,Title: Mitogenic activation of human T cells induces two closely related genes which sh
A,Reference number: A30574; MUID:89140347; PMID:2521882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-92 C21P>
A; Cross-references: GB MZ5315; NID:g602452; PIDN:AAA57255.1; PID:g602453
A; By Blum, S.; Forsdyke, R.E.; Forsdyke, D.R.
DNA cell Biol. 9, 589-602, 1990
A; Fille: Three human homologs of a murine gene encoding an inhibitor of stem cell prolife
A; Reference number: A30412; MUID:91103879; PMID:2271120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: A30412
A;Molecule type: mRNA
A;Residues: 1-92 <BLD.
A;Residues: 1-92 <BLD.
A;Cross-references: GB:M23178; GB:M32337; NID:g182846; PIDN:AAA35858.1; PID:g182847
B;Obaru, K.; Fukuda, M.; Maeda, S.; Shimada, K.
J. Biochem., 99, 885-894, 1986
A;Title: A CDNA clone used to Study mRNA inducible in human tonsillar lymphocytes by a transference number: A24198; MUID:86223879; PMID:3086300
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N;Alternate names: H400; SIS gamma; T-cell activation protein gamma
C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1989 #sequence revision 28-Aug-1989 #text_change 09-Jul-2004
C;Accession: C30552; JL0088; FS0304; S22042
R;Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
A;Immunol. 142, 679-687; 1989
A;Title: A family of small inducible proteins secreted by leukocytes are members of a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P14097; GB:M23503; NID:g533244; PIDN:AAA40148.1; PID:g533245 R;Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; Davatelis, G.; Wolpe, S.D.; Masi Job., 2251-2259, 1988
A;Title: Resolution of the two components of macrophage inflammatory protein 1, and cloni A;Reference number: JL0088; MUID:89067830; PMID:3058856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: CDB:120368; OMIM:182283
A;Map position: 17q11-17q21
C;Superfamily: macrophage inflammatory protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-92/Product: macrophage inflammatory protein 1-alpha #status predicted <MAT>
F;31-52/Product: macrophage #status predicted conds: #status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:X03754; NID:g34298; PIDN:CAA27388.1; PID:g758089 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 92;
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A;Reference number: A30552; MUD:89093958; PMID:2521353
A;Accession: C30552
A;Molecule type: mRNA
A;Residues: 1-92 <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
46.8%; Score 236; DB 2;
Best Local Similarity 48.4%; Pred. No. 5.2e-19;
Matches 44; Conservative 22; Mismatches 23.
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                                                      A; Molecule type: DNA
A; Residues: 1-92 <NAK>
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-92 <OBA>
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A; Molecule type: mRNA
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A30574
macrophage inflammatory protein 1-alpha precursor - human
N;Alternate names: LD78-alpha protein precursor; lymphocyte tumor promoter-induced prote
tivation protein 1
C;Species: Homo sapiens (man)
C;Date: 03-Aug-1992 #sequence revision 03-Aug-1992 #text_change 09-Jul-2004
C;Accession: A35673; A30574; A30412; A24198; A30908
R;Nakao, M.; Nomiyama, H.; Shimada, K.
Mol. Cell Biol. 10, 3646-3658, 1990
A;Title: Structures of human genes coding for cytokine LD78 and their expression.
A;Reference number: A35673; MUID:90287155; PMID:1694014
                                                                                                                                                 RESULT 1
B13673
LD78-beta protein precursor - human
N/Alternate names: macrophage inflammatory protein homolog GOS19-2; small inducible cytc
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: B35673; B30412; S10157; B30908
R;Nakao, M.; Nomiyama, H.; Shimada, K.
R;Nakao, M.; Nomiyama, H.; Shimada, K.
A;Title: Structures of human genes coding for cytokine LD78 and their expression.
A;Reference number: A35673; MUID:90287155; PMID:1694014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-93 <NAKA
DNA Cell Biol. 9, 589-602, 1990
DNA Cell Biol. 9, 589-602, 1990
A; Title: Three human homologs of a murine gene encoding an inhibitor of stem cell prolif
A; Reference number: A30412; MUID:91103879; PMID:2271120
A; Accession: B30412
A; Residues: Preliminary; not compared with conceptual translation
A; Residues: 1-93 <-BUA
A; Residues: 1-94 <-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M24110; GB:M32338; NID:g182848; PIDN:AAA35859.1; PID:g182849
R;Irving, S.G.; Zipfel, P.F.; Balke, J.; McBride, O.W.; Morton, C.C.; Burd, P.R.; Sieben
Nucleic Acids Res. 18, 3261-3270, 1990
A;Title: Two inflammatory mediator cytokine genes are closely linked and variably amplif
A;Reference number: S10157; MUID:90287702; PMID:1972563
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: mRNA
A,Residues: 1-93 <IRV>
A,Cross-references: EMBL:X52149; NID:g34750; PIDN:CAA36397.1; PID:g296666
C,Comment: This protein is a member of a "small inducible" or "activation specific" gene
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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47.7%; Score 240.5; DB 2; Length 93;
Best Local Similarity 47.3%; Pred. No. 1.7e-19;
Matches 43; Conservative 22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Superfamily: macrophage inflammatory protein
C.Keywords: cytokine
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-93/Product: LD78-beta protein #status predicted <MAT>
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A; Introns: 26/1; 64/2
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A; Status: preliminary
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C;Accession: JH0319; A40978; A31767; A37411; B30574; B45817; D30552
R;Baixeras, E.; Roman-Roman, S.; Jitsukawa, S.; Genevee, C.; Mechiche, S.; Viegas-Pequigr Mol. Immunol. 27, 1091-1102, 1990
A;Title: Cloning and expression of a lymphocyte activation gene (LAG-1).
A;Reference number: JH0319; MUID:91061800; PMID:2247088
                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: UNIPROT:P13236; GB:X53682; NID:g34217; PIDN:CAA37723.1; PID:g34218
A,Experimental source: natural killer cell, strain CD3-CD2+, F5, 51IIE5
K,Napolicano, M.; Modi, W.S.; Cevario, S.J.; Gnarra, J.R.; Seuanez, H.N.; Leonard, W.J.
J. Biol. Chem. 266, 17531-17536, 1991
A,Title: The gene encoding the Act-2 cytokine. Genomic structure, HTLV-I/tax responsivene A,Reference number: A40978; MUID:9137378; PMID:1894635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Modecule type: mRNA
A; Residues: 1-92 < CHA>
A; Residues: 1-92 < CHA>
A; Cross-references: GB:X16166; NID: 932035; PIDN: CAA34291.1; PID: 932036
R; Zipfel., P.F.; Balke, J.; Irving, S.G.; Kelly, K.; Siebenlist, U.
J. Immunol. 142, 1582-1590, 1989
A; Title: Mitogenic activation of human T cells induces two closely related genes which shareference number: A30574; MUID: 89140347; PMID: 2521882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residues; Comment: This protein is secreted by activated lymphocytes and monocytes. It is bound 1
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R;Chang, H.C.; Reinherz, B.L.
Ex. J. Tamunol. 19, 1045-1051, 1989
A;Title: Isolation and characterization of a cDNA encoding a putative cytokine which is A;Reference number: A37411; MUID:89325421; PMID:2568930
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A,Residues: 7-55, I',57-79,'T',81-92 cMIL>
A,Residues: 7-55, I',57-79,'T',81-92 cMIL>
A,Cross-references: GB:MS7503; NID:g339726; PIDN:AAA36752.1; PID:g339727
R,Erown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
J. Immunol. 142, 679-687, 1989
A,Title: A family of small inducible proteins secreted by leukocytes are members of a for various activation processes.
A,Reference number: A30552; MUD:89093958; PMID:2521353
A,Reference number: A30552; MUD:89093958; PMID:2521353
A,Rolecule type: mRNA
A,Rolecule type: mRNA
A,Rolecule type: GB:M23502; NID:9533212; PIDN:AAA36656.1; PID:g533213
B,Cross-references: GB:M23502; NID:9533212; PIDN:AAA36656.1; PID:g533213
B,Cross-references: GB:M23502; NID:g533212; January 1994
A,Reference number: A52206; PDB:IHUM
A,Reference number: A52206; PDB:IHUM
A,Reference number: A52206; PDB:IHUM
A,Reference number: A52206; PDB:IHUM
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Proc. Natl. Acad. G21. U.S.A. 85, 9704-9708, 1988
Affitle: Identification, cloning, and characterization of an immune activation gene.
A;Reference number: A31767; MUID:89071764; PMID:2462251
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A; Residues: 1-19, 'L', 21-92 <ZIP>
A; Residues: 1-19, 'L', 21-92 <ZIP>
A; Cross-references: GB: M25316; NID: g602454; PIDN: AAA57256.1; PID: g602455
R; Miller: M.D.; Hata, S.; Malefyt, R.D.W.; Krangel, M.S.
J. Immunol. 143, 2907-2916, 1989
A; Title: A novel polypeptide secreted by activated human T lymphocytes.
A; Reference number: A45817; MUID: 90038522; PMID: 2809212
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A; Mesidues 1.14, 'S', 16-69, 'G', 71-92 «NAP>
A; Cross-references: GB: M69201; NID: 9178021
A; Note: 15-Ala was also found
                                                                                                                                                                                                                                                        A; Status: translation not shown
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A;Introns: 26/1; 64/2
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A; Residues: 1-92 <BAI>
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A; Residues: 1-92 <LIP>
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A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-92 <MOR>
A.Cross-references: UNIPROT:P46632; GB:D17402; NID:g599577; PIDN:BAA04226.1; PID:g599578
C.Superfamily: macrophage inflammatory protein
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macrophage inflammatory protein 1-beta precursor [validated] - human
macrophage inflammatory protein 1-beta precursor [validated] - human
N;Alternate names: cytokine HC21; G-26 protein; H400 homolog; lymphocyte activation gene
protein 2 (Act-2); T-cell activation protein gamma
C;Species: Homo sapiens (man)
C;Species: 07-Jun-1990 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
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A; Residues: 1-92 <SHE>
A; Cross-references: GB:M35590; NID:g199696; PIDN:AAA39708.1; PID:g199697
A; Accession: B0304
A; Molecule type: protein
A; Residues: 24-33, 'XX', 36, 'X', 38 <SH2>
A; Residues: 22042
A; Reference number: S22042
A; Residues: 1-92 <ABA>
A; References: EMBL:X62502; NID:g53126; PIDN:CAA44364.1; PID:g53127
C; Comment: This protein is a monokine.
C; Comment: This protein is a monokine.
C; Comment: S6/1; 64/2
C; Reywords: g1ycoprotein
F; 1-23/Domain: signal sequence #status predicted <SIG>F; A-92/Product: macrophage inflammatory protein 1-beta #status experimental <AMAT>
F; A-92/Product: macrophage inflammatory protein 1-beta #status predicted
F; 76/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: 146730
R;Mori, S.; Goto, R.; Goto, F.; Mutakami, K.; Ohkawara, S.; Yoshinaga, M. Int. Immunol. 6, 149-156, 1994
A;Title: Dynamic changes in mRNA expression of neutrophils during the course A;Reference number: 146730; MUID:94198229; PMID:8148323
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A Molecule type: protein
A;Molecule type: protein
A;Residues: 24-33, XX,'36-42 < WOL>
A;Residues: 24-33, XX,'36-42 < WOL>
A;Note: 26-Met, 30-Pro, and 39-Thr were also found
B;Widmer, U.; Yang, Z.; van Deventer, S.; Manogue, K.R.; Sherry, B.; Cerami, A.
J. Immunol. 146, 4031-4040, 1991
A;Fitle: Genomic structure of murine macrophage inflammatory protein-1-alpha and conserve
A;Reference number: 156104; MUID:91237116; PMID:2033269
                                                    A;Residues: 24-33,'XX',36-54 <SHE>
R;Wolpe, S.D.; Davatelis, G.; Sherry, B.; Beutler, B.; Hesse, D.G.; Nguyen, H.T.; Moldawe
J. Exp. Med. 167, 570-581, 1988
                                                                                                                                                                                                                A,Title: Macrophages secrete a novel heparin-binding protein with inflammatory and neutro
A,Reference number: A27596; MUID:88154745; PMID:3279154
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Superfamily: macrophage inflammatory protein
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C;Keywords: heparin binding
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-92/Product: macrophage inflammatory protein #status experimental <MAT>
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A;Cross-references: GB:M73061; NID:g199694; PIDN:AAA39707.1; PID:g199695
C;Comment: This protein is a monokine.
C;Genetics:
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Best Local Similarity 45.2%; Pred. No. 1.4e-17;
Matches 42; Conservative 21; Mismatches 28; Indels
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45.2%; Pred. No. 1.4e-17;
cive 22; Mismatches 27
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A,Molecule type: DNA
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nes 42; Conservative
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                                                                                                                                                                                                                                                                                                                                    A; Accession: A27596
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A, Residues: 1-92 <GRO>
A, Residues: 1-92 <GRO>
A, Residues: 1-92 <GRO>
A, Residues: 1-92 <GRO>
A, Cross-references: UNIPROT: P10855; EMBL: X53372; NID: 954062; PIDN: CAA37452.1; PID: 929753
A, Moles: the authors' translation of the nucleotide sequence differs at several positions R; Kwon, B.S.; Weissman, S.M.
B, Kwon, B.S.; Weissman, S.M.
Broc. Natl. Acad. Sci. Us.A. 86, 1953-1967, 1989
A, Accession: A32393; MUD: 89184547; PMID: 2784565
A, Reference number: A32393; MUD: 89184547; PMID: 2784565
A, Residues: 1-92 <KWO>
A, Residues: 1-92 <KWO>
A, Residues: 1-92 <KWO>
A, Residues: 1-92 <KWO
A, 
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NyAlternate names: heparin-binding chemotaxis protein; L2G25B protein; SCI/MIP-1a; SIS a
C;Species: Mus musculus (house mouse)
C;Dacies: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text change 09-Jul-2004
C;Accession: S11685; A32393; A3885; A38552; PS0303; A27596; I56104
R;Grove, M.; Lowe, S.; Graham, G.; Pragnell, I.; Plumb, M.
Aviclaic Acids Res. 18, 5561, 1990
A;Title: Sequence of the murine haemopoietic stem cell inhibitor/macrophage inflammatory
A;Reference number: S11685; MUID:91016858; PMID:2216738
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A; Regidues: 1-21, 'L', 23-61,'A', 63-92 < BRO>
A; Regidues: 1-21,'L', 23-61,'A', 63-92 < BRO>
A; Cross-references: GB: M23447; NID: 9533240; PIDN: AAA40146.1; PID: 9533241
B; Sheamp-Ollason, P.; Gallegos, C.; Bauer, D.; Davatelis, G.; Wolpe, S.D.; Mas J. Exp. Med. 168, 2251-2259, 1988
A; Title: Resolution of the two components of macrophage inflammatory protein 1, and clor A; Reference number: JL0088; MUID: 89067830; PMID: 3058856
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A; Residues: 1-48, E',50-90,'I',92 < DA2>
A; Residues: 1-68, E',50-90,'I',92 < DA2>
A; Cross-references: EMBL:X12531
A; Note: the authors translated the codon GAG for residue 49 as Asp and ATT for residue
A; Note: the sequence has been corrected in reference A53885
B; Davatelis, G; Tekamp-Olson, P; Wolpe, S.D; Hermsen, K; Luedke, C; Gallegos, C;
J; Exp. Med. 170, 2189, 1989
A; Reference number: A53885
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R;Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
J. Immunol. 142, 679-687, 1989
A;Titler A family of small inducible proteins secreted by leukocytes are members of so various activation processes.
A;Reference number: A30552; MUID:89093958; PMID:2521353
                                                    F;24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>
F;34-58,35-74/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                      44.5%; Score 224.5; DB 1; Length 43.0%; Pred. No. 9.7e-18; Live 20; Mismatches 32; Indels
F;1-23/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                    40; Conservative
                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                          Matches
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C;Accession: JE0177
R;Youn, B.S.; Zhang, S.; Broxmeryer, H.E.; Antol, K.; Fraser Jr., M.J.; Hangoc, G.; Kwon, Biochem. Biophys. Res. Commun. 247, 217-222, 1998
A;Title: Isolation and characterization of LMC, a novel lymphocyte and monocyte chemoatt: A;Reference number: JE0177; MUID:98308096; PMID:9642106
A;Accession: JE0177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: 149555
R;Orlofsky, A.; Berger, M.S.; Prystowsky, M.B.
R;Orlofsky, A.; Berger, M.S.; Prystowsky, M.B.
A;Title: Novel expression pattern of a new member of the MIP-1 family of cytokine-like ge A;Reference number: 149555; MUID:91370083; PMID:1832565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P27784; GB:M58004; NID:g192243; PIDN:AAA37329.1; PID:g192244
                                                                                                                                                                                                                                            C, Superfamily: macrophage inflammatory protein
C, Superfamily: macrophage inflammaton
C, Superfamily: cytokine; immediate-early protein; inflammation
E, 1-23/Domain: signal sequence #status predicted <SIG>
F; 1-23/Domain: signal sequence #status cytokine RANTES #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKISVAAIPFFLLITIALGTKTESSSRGP---YHPSECCFTYTTYKIPRQRIMDYYETNS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lymphocyte and monocyte chemoattractant CC chemokine - human
C;Species: Homo sapiens (man)
C;Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKISVAAIPFFLLITIALGTKTESSSRGPY - - HPSECCFTYTTYKIPRQRIMDYYETNSQ
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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A;Reference number: 156970; MUID:92277990; PMID:1375672
A;Accession: 156970
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42.4%; Pred. No. 4.4e-13;
iive 15; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                 37.5%; Score 189; DB 1;
ilarity 42.7%; Pred. No. 8.2e-14;
Conservative 15; Mismatches 30;
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A;Molecule type: mRNA
A;Residues: 1-116 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 QCSKPGIVFITKRGHSVCTNPSDKWVQDYIKD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 NCHLPAIIFVTKRNREVCTNPNDDWVQEYIKD 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 CSKPGIVFITKRGHSVCTNPSDKWVQDYI 87
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                                                  A;Status: translated from GB/EMBL/DDBJ
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 39; Conserv
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A; Residues: 1-120 < YOU>
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                                                                                                                                                                                            C; Genetics:
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                                                                                                                M.M.; Kz
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A) Cross-references: 1-31. UNIPROT: P30882; EMBL: U02298; NID: 9460090; PIDN: AAA18302.1; PID: 94600 R; Schall, T.J.; Simpson, N.J.; Mak, J.Y.

Eur. J. Immunol. 22, 1477-1481, 1992

Eur. J. Immunol. 22, 1477-1481, 1992

A; Title: Molecular cloning and expression of the murine RANTES cytokine: structural and A; Reference number: A46539; MUID: 92288805; PMID: 1376260

A; Accession: A46539

A; Molecule type: mRNA

A; Residues: 1-18, A', 20-91 <8CH>
A; Residues: 1-18, A', 20-91 c8CH>
A; Experimental source: mRNA

A; Residues: GB: S37648; NID: 9250207; PIDN: AAB22330.1; PID: 9250208

A; Cross-references: GB: S37648; NID: 9250207; PIDN: AAB22330.1; PID: 9250208

A; Cross-reference extracted from NCBI backbone (NCBIN: NCBIP: 106770)

R; Shin, H.S.; Drysdale, B.E.; Shin, M.L.; Noble, P.W.; Fisher, S.N.; Paznekas, W.A.

Mol. Cell. Biol. 14, 2914-2925, 1994

A; Patitle: Definition of a lipopolysaccharide-responsive element in the 5'-flanking region A; Accession: 148654; MUID: 94217689; PMID: 7513046

A; Accession: Label and A; All and A; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Wolecule type: mRNA
A; Residues: 1-91 - SCH->
A; Cross-references: UNIPROT: P13501; GB: M21121
C; Comment: The acronym RANTES reflects the description "Regulated upon Activation, Norma
C; Genetics:
A; Gene: GDB: SCYAS; D178136E
A; Cross-references: GDB: 120749; OMIM: 187011
A; Map position: 17911.2-17912
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Monocyte chemoattractant cytokine RANTES precursor - mouse
N;Alternate names: MuRantes
N;Alternate names: MuRantes
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus 1993 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: 148875; A46539; I48654; I56970
R;Danoff, T.M.; Lalley, P.A.; Chang, Y.S.; Heeger, P.S.; Neilson, E.G.
J;Immunol. 152, 1182-1189, 1994
A;Title: Cloning, genomic organization, and chromosomal localization of the Scya5 shifted number: 148875; MUID:94132613; PMID:7507961
NiAlternate names: small inducible cytokine A5; T-cell specific cytokine RANTES C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 3.0-Jun-1989 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C; Accession: A28815
R; Schall, T.J.; Jongstra, J.; Dyer, B.J.; Jorgensen, J.; Clayberger, C.; Davis, J. Immunol. 141, 1018-1025, 1988
A; Title: A human T cell-specific molecule is a member of a new gene family.
A; Reference number: A28815, MUID:88285659; PMID:2456327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   finey foretamily: macrophage inflammatory protein
C;Superfamily: macrophage inflammatory immediate-early protein; inflammation; T-cell
C;Keywords: chemotaxis; cytokine; immediate-early protein; inflammation; T-cell
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-91/Product: T-cell protein RANTES #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKVSAAALAVILIATALCA----PASASPÝSSDTTPCCFAYIARPLPRAHIKEÝFYTSGK 56
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; Pred. No. 4.9e-14;
18; Mismatches 35;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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36.6%;
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Best Local Similarity 36.6*
Matches 34; Conservative
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A; Residues: 1-91 <SHI>
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Query Match
Best Local Si
Matches 33;
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J. Immunol. 144, 4434-4441, 1990
A. Timmunol. 164, adherence results in selective induction of novel genes sharing homolo A;Reference number: A60407; MUID:90257367; PMID:2341726
A;Accession: C60407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monocyte chemoattractant protein-1 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: 146857
R;Yoshimura, T.; Yuhki, N.
A;Title: Naturophil attractant/activation protein-1 and monocyte chemoattractant protein
A;Reference number: 146857; MUID:91225489; PMID:2026877
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A;Cross-references: UNIPROT:P28292; GB:M57440; NID:g165469; PIDN:AAA31386.1; PID:g165470
C;Superfamily: macrophage inflammatory protein
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                                                                                                           1 MKVS-ATLLCLLLIAVAFSSHVLAQPDAVNSPVTCCYTFTNKTISVKRLMSYRRINSTKC 59
                                                                                     1 MKISVAAIPFFLLITIALGTKT-----ESSSRGPYHP-----SECCFTYTTYK 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNS-QC 59
                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C;Accession: C60407
                                               Gaps
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                                            20;
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b; Pred. No. 5.1e-10;
17; Mismatches 40; Indels
  35.7%; Score 180; DB 2; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-50 <SPO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.3%; Score 163; DB 2; Length 50; larity 52.0%; Pred. No. 3.5e-11; Conservative 12; Mismatches 12; Indels
                    ; Pred. No. 1e-12;
22; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: 146857
A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monocyte chemoattractant protein-1 precursor - pig
(;Species: Sus scrofa domestica (domestic pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 SKPGIVFITKRGHSVCTNPSDKWVQDYIKDM 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 PKEAVIFMTKLAKGICADPKQKWVQDAIANL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT: Q8NHW4 superfamily: macrophage inflammatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.0%;
35.2%;
                      37.6%;
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Best Local Similarity 35.2%
                                          41; Conservative
Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C;Accession: JC2136; S57498
R;Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
Biochem: Biophys. Res. Commun. 199, 962-968, 1994
A;Title: Porcine luteal cells express monocyte chemoatractant protein-1 (MCP-1): Analysi A;Reference number: JC2136; MUID:94183284; PMID:7510962
A;Accession: JC2136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rivan Coillie, E.; Froyen, G.; Nomiyama, H.; Miura, R.; Fiten, P.; Van Aelst, I.; Van Dan Biochem. Biophys. Res. Commun. 231, 726-730, 1997
Affitle: Human monocyte chemotactic protein-2: CDNA cloning and regulated expression of n A, Reference number: JC5295; MUID:97224420; PMID:9070881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: JC5295
A;Molecule type: mRNA
A,Rosidues: 1-99 < VAN>
A;Cross-references: UNIPROT:P80075; GB:Y10802; NID:g1924937; PIDN:CAA71760.1; PID:g192493:
A;Experimental source: bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Comment: This protein belongs to the beta-chemokine family which is one of the major HI tis and in tumor biology, and contribute to the trafficking and recuitment of the respons
                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-99 <HOS>
A;Cross-references: UNIPROT:P42831; GB:Z48479; NID:g683716; PIDN:CAA88370.1; PID:g683717
R;Zach, O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: EMBL:X79416; NID:g872312; PIDN:CAA55945.1; PID:g8723133 C; Superfamily: macrophage inflammatory protein C; Keywords: glycoprotein C; Keywords: glycoprotein F;1-23/Domain: signal sequence #status predicted <SIG>F;1-29/Product: moncoyte chemoattractant protein-1 #status predicted <MAT>F;24-99/Product: moncoyte chemoattractant protein-1 #status predicted <MAT>F;94/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monocyte chemotactic protein-2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JC2295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKISVAAIPPFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYB-TNSQC
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C;Superfamily: macrophage inflammatory protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-99/Product: monocyte chemotactic protein-2 #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 30.5%; Score 153.5; DB 2; Local Similarity 37.9%; Pred. No. 7.6e-10; les 36; Conservative 14; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKEAVIFKTIAGKEICAEPKOKWVODSISHLDKKN 94
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35.5%; Pred. No. 1.4e-09;
tive 16; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 SKPGIVFITKRGHSVCTNPSDKWVQDYIKDM-KEN 93
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                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, July 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: S57497
A;Accession: S57498
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-99 <ZAC>
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monocyte chemoattractant protein 1 precursor - bovine
NyAlternate names: monocyte chemotactic factor 1; seminal plasma protein P6
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A39296; B39296
C;Accession: A39296; B39296
B;Wempe, F;Henschen, A.; Scheit, K.H.
DNA Cell Biol. 10, 671-679, 1991
A;Title: Gene expression and cDNA cloning identified a major basic protein constituent of A;Reference number: A39296; MUID:92096117; PMID:1721821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-99 <WEM>
A;Cross-references: UNIPROT:P28291; GB:M84602; GB:M85264; NID:g163394; PIDN:AAA30651.1;
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R; Wempe, F.; Kuhlmann, J.K.; Scheit, K.H.
Biochem. Biophys. Res. Comuun. 202, 1272-1279, 1994
A; Title: Characterization of the bovine monocyte chemoattractant protein-1 gene. A; Reference number: JC2336; MUID:94338337; PMID:8060303
                                                                                                                                                                                                               1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYE-TNSQC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKVS-AALLCLLITVAAFSTEVLAQPDAINSQVACCYTFNSKKISMQRLMNYRRVTSSKC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    monocyte chemoattractant protein-1 - bovine
C;Species: Bos primigenius indicus (zebu cattle)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #status predicted <MAT>
                                                                                                                                                                  1 MKISVAAIPFELLITI-ALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYE-TNSQ
                                                                                         Gaps
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F1-123/Domain: signal sequence #status predicted <SIG>
F:24-99/Product: monocyte chemoatrzactant protein 1 #status predict
F:94/Binding site: carbohydrate (Asn) (covalent) #status predicted
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            Length 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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        29.6%; Score 149; DB 1;
llarity 33.7%; Pred. No. 3.6e-09;
Conservative 20; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                     CPKEAVVFVTKLKREICADPNKEWVQKYIRKLDQN 93
                                                                                                                                                                                                                                                                                                                        CSKPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
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29.5%; Score 148.5; DB 1

Best Local Similarity 36.8%; Pred. No. 2.7e-09;

Matches 35; Conservative 17; Mismatches 40
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C;Superfamily: macrophage inflammatory protein
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A;Residues: 50-68,'X',70-74,'X',76 <WE2>
A;Experimental source: seminal vesicle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 35; Conserv
                                                Similarity
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Query Match
Best Local Simi
Matches 32;
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                                        PAGE inducible JE glycoprotein precursor - mouse

PDGF-inducible JE glycoprotein precursor - mouse

PDGF-inducible JE glycoprotein precursor - mouse

C; Species: Mus musculus (house mouse)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C; Accession: A30209; A44771; A30861

R; Rollins, B.J.; Morrison, E.D.; Stiles, C.D.

Proc. Natl. Acad. Sci. U.S.A. 85, 3738-3742, 1988

A; Riberance number: A30209; MUID:88234501; PMID:3287374

A; Reference number: A30209

A; Molecule type: DNA

A; Residues: 1-148 &ROL.

A; Cross-references: UNIPROT:P10148; GB:M19681; NID:g193486; PIDN:AAA37684.1; PID:g387168

R; Kawahara, R.S.; Deutel, T.F.

G; Biol. Chem. 264, 679-662, 1999

A; Title: Platelet-derived growth factor-inducible gene JE is a member of a family of sma A; Reference number: A44771; MUID:89093129; PMID:2910858
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S07723; JN0128
Nucleic Acids Res. 18, 23-34, 1990
Nucleic Acids Res. 18, 23-34, 1990
Nucleic Acids Res. 18, 23-34, 1990
A;Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential A;Reference number: S07723; MUID:90174947; PMID:2106664
A;Accession: S07723
A;Accession: S0
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A;Cross-references: GBS.M57441; NID:g205333; PIDN:AAA63496.1; PID:g205334
A;Experimental source: spleen cells
A;Note: the authors translated the codon GAA for residue 62 as Lys and GCT for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Introns: 26/1; 65/2
C;Superfamily: macrophage inflammatory protein
P;1-23/Domain: signal sequence #status predicted <SIG>
F;24-148/Product: immediate-early serum-responsive protein JE #status predicted <MAT>
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: macrophage inflammatory protein
C;Keywords: cytokine; glycoprotein
F;126/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.9%; Score 150.5; DB 1 41.3%; Pred. No. 2.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
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Best Local Similarity 41.3
Matches 26; Conservative
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A; Residues: 1-148 <KA2>
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A; Title: Porcine luteal cells express monocyte chemoattractant protein-2 (MCP-2): Analysi A; Reference number: JC2417; MUD:95091716; PMID:7999015
A; Accession: JC2417
A; Molecule type: mRNA
A; Residues: 1-99 < HOSA
A; Residues: 1-99 < HOSA
A; Residues: 1-99 cence: Corpus luteum
A; Experimental source: corpus luteum
C; Superfamily: macrophage inflammatory protein
F; 1-23/Domain: signal sequence #status predicted <SIG>F; 24-99/Product: monocyte chemoattractant protein-2 #status predicted <MAT>
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C.Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C.Species: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C.Species: 01-Schlueter, C.; Richter, E.; Noso, N.; Kulke, R.; Christophers, E.; Schroer
Biochem. Biophys. Res. Commun. 225, 1045-1051, 1996
A; Ritle: Human dermal fibroblasts express eotaxin: Molecular cloning, mRNA expression, ar
A; Reference number: JC4912
A; Reference number: JC4912
A; Residues: 1-97 cbaR>
A; Repertemalal source: dermal fibroblast
C; Comment: This protein has eosinophil specific chemotatic activity.
C; Superfamily: macrophage inflammatory protein
C; Reywords: fibroblast
F; 1-18/Domain: signal sequence #status predicted cMAT>
F; 19-97/Product: eotaxin #status predicted cMAT>
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A,Title: Exctaxin: Cloning of an eosinophil chemoattractant cytokine and increased mRNA eshaceseion: JC2478; MUID:95091818; PMID:7999113
A,Reference number: JC2478
A,Reference Type: MRNA
A,Redeule type: M
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 16-Jul-1999
C;Accession: JC2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MOVS-AALLCLLTTAAFSTQVLAQPDSVSIPITCCFGLVNGKIPFKKLESYTRITNSQC
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C. Date: 21, 403-408, J094
R. Opdenakker, G.; Fiten, P.; Nys, G.; Froyen, G.; Van Roy, N.; Speleman, F.; Laureys, G. Ropension: A54678; MUID:94375065; PMID:7916328
A. A. Reference number: A54678; MUID:94375065; PMID:7916328
A. A. Residues: 1-109 ADD
A. Reference number: AC1478; MUID:93213290; PMID:8461011
A. Accession: AC1478; MUID:93213290; PMID:8461011
A. Accession: AC1478; MUID:93213290; PMID:8461011
A. Accession: AC1478; MUID:93213290; PMID:9328270; PIDN:CAAS1055.1; PID:9313708
A. Chalon, P.; Guillemot, J.C.; Kaghad, M.; Liauzun, P.; Magazin, M.; Miloux, submitted to the EMBL Data Library, March 1993
A. Reference number: S32222
A. Reference number: S32222
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A.Molecule type: mRNA
A.Molecule type: mRNA
A.Resdues: 1-109 <MIN>
A.Cross-references: EMBL:X71087; NID:g288396; PIDN:CAA50405.1; PID:g288397
C.Comment: This protein induces proteinase secretion and chemotaxis by macrophages and
C.Genetics: This protein induces proteinase secretion and chemotaxis by macrophages and
A.Gene: GDB:SCYA7; SCYA6; MCP-3
A.Cross-references: GDB:138473; OMIM:158106
A.A.Map position: 17411-17412
A.Introns: 36/1; 75/2
C.Superfamily: macrophage inflammatory protein
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JOCAL7
monocyte chemoattractant protein-2 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C;Accession: JC2417
C;Accession: JC;All
R;Hosang, K:; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 205, 148-153, 1994
                 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYE-TNSQC
                                                                                                      1 MKVS-AALLCLLITVAAFSTEVLAQPDAINSQVACCYTFNSKKISMQRLMNYRRVTSSKC
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Pred. No. 5.7e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 20
A54678
Monocyte chemotactic protein 3 precursor - human
N;Alternate names: monocyte chemoattractant protein MCP-3
                                                                                                                                                                                                                                               60 SKPGIVFITKRGHSVCTNPSDKWVQDYIKDM-KEN
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A;Cross-references: GB:M30816; GB:M31625; GB:M31626; NID:g188701; PIDN:AAA36330.1; PID:g:RyOshimura, T.; Yuhki, N.; Moore, S.K.; Appella, E.; Lerman, M.I.; Leonard, B.J. FEBS Lett. 244, 487-493, 1989
FABS Lett. 244, 487-493, 1989
A;Title: Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, expa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross_references: GB:S71513; NID:g240867; PIDN:AAB20651.1; PID:g240868
R;Bottazzi, B.; Colotta, F.; Sica, A.; Nobili, N.; Mantovani, A.
Int. J. Cancer 45, 795-797, 1990
A;Title: A chemoattractant expressed in human sarcoma cells (tumor-derived chemotactic fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Reference number: A60299; MUID: 90216082; FMID: 2182547
A; Reference number: A60299
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-99 < BOT>
B; Furutani, Y:; Nomura, H.; Notake, M.; Oyamada, Y.; Fukui, T.; Yamada, M.; Larsen, C.G.,
B; Furutani, Y.; Nomura, H.; Notake, M.; Oyamada, Y.; Fukui, T.; Yamada, M.; Larsen, C.G.,
A; Fille: Cloning and sequencing of the cDNA for human monocyte chemotactic and activating
A; Reference number: A32300; MUID: 89165862; PMID: 2923622
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A; Residues: 1-99 < FUR>
A; Cross -references GB: M24545; NID: 9187434; PIDN: AAA18164.1; PID: 9307163
A; Cross -references GB: M24545; NID: 9187434; PIDN: AAA18164.1; PID: 9307163
A; Risbinson, B.A.; Yoshimura, T.; Leonard, E.J.; Tanaka, S.; Griffin, P.R.; Shabanowitz, L. Proc. Natl. Acad. Sci. U.S.A. 86, 1850-1854, 1989
A; Title: Complete amino acid sequence of a human monocyte chemoattractant, a putative mec A; Reference number: A32396; MUID: 89184525; PMID: 2648385
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: Drotein
A; Molecule type: Commun. 167, 904-909, 1990
A; Dicchem. Biophys. Res. Commun. 167, 904-909, 1990
A; Title: Identification of the monocyte chemotactic protein from human osteosarcoma cells
A; Reference number: A34561; MUID: 90211336; PMID: 2322286
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Mesidues: 29-33, 'XX', 36-52;82-92 <DEC>
A;ELi, Y.S.; Shyy, Y.J.; Wright, J.G.; Valente, A.J.; Cornhill, J.F.; Kolattukudy, P.E.
Mol. Cell. Biochem. 126, 61-68, 1993
A;Title: The expression of monocyte chemotactic protein (MCP-1) in human vascular endothe A;Reference number: 157488; MUID:94150478; PMID:8107690
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R;Ye, Q.N.; Su, G.F.; Yuan, Y.; Huang, C.F.
Chinses J. Microbiol. Immunol. 14, 29-32, 1994
A;Title: The PCR, cloning and sequencing of human monocyte chemoattractant protein-1 (MCI A;Reference number: JC1096
                                                                                                                                                                                                                                                                                               A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-96 ×705.
A; Cross-references: GB:X14768; NID:g34513; PIDN:CAA32876.1; PID:g34514
A; Experimental source: glioma cell line U-105MG
R; Yoshimura, T.; Leonard, B.J.
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A; Title: Human monocyte chemoattractant protein-1 (MCP-1).
A; Reference number: I51841; MUID:92095166; PMID:1661560
                                                                                                                                                                                                                         A; Reference number: S03339; MUID:89153605; PMID:2465924
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A;Molecule type: mRNA
A;Residues: 1-99 <LIY>
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A,Residues: 24-28,'Q',30-99 <YEQ>
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A;Map position: 17q11.2-17q12
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A; Residues: 1-99 < YO2>
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C;Species: Cavia porcellus (guinea pig)
C;Dacession: 148099
F;Rothenberg, M.E.; Iuster, A.D.; Lilly, C.M.; Drazen, J.M.; Leder, P.
F;Rothenberg, M.E.; Iuster, A.D.; Lilly, C.M.; Drazen, J.M.; Leder, P.
J. Exp. Med. 181, 1211-1216, 1995
A;Title: Constitutive and allergen-induced expression of ectaxin mRNA in the guinea pig
A;Reference number: 148099; MUID:95173589; PMID:7869037
A;Accession: 148099
A;Accession: 148099
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-96 «RES.
A;Cross-references: UNIPROT:P80125; EMBL:U18941; NID:9687655; PIDN:AAC52180.1; PID:96876
C;Superfamily: macrophage inflammatory protein
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monocyte chemoattractant protein 1 precursor - human
NyAlternate names: GDCF-1; glioma-derived monocyte chemotactic factor 1; MCAF; MCP-1; mc
N;Contains: glioma-derived chemotactic factor 2 (GDCF-2)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 09-Jul-2004
C;Accession: A35474; A33476; S03339; IS1841; A60299; A32300; A32366; A34561; IS7488; JC1
R;Shyy, Y.J.; Li, Y.S.; Kolattukudy, P.E.
Biochem. Blophys: Res. Commun. 169, 346-351, 1990
A;Title: Structure of human monocyte chemotactic protein gene and its regulation by TPA.
A;Accession: A35474; MUID:90290466; PMID:2357211
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A; Residues: 1-99 <SHY>
A; Residues: 1-99 <SHY>
A; Cross-references: UNIPROT: P13500; GB: M37719; NID: g187447; PIDN: AAA18102.1; PID: g487124
A; Cross-references: UNIPROT: P13500; GB: M37719; NID: g187447; PIDN: AAA18102.1; PID: g487124
B; Rollins, B.J.; Stier, P.; Ernst, T.; Wong, G.G.
Mol. Cell. Biol. 9, 4687-4695, 1989
A; Title: The human homolog of the JE gene encodes a monocyte secretory protein.
A; Reference number: A33476; MUID: 90097880; PMID: 2513477
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Best Local Similarity 37.2*
Matches 32; Conservative
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A; Molecule type: mRNA
A; Residues: 1-99 <ROL>
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A,Gene: GDB:SCYA1; 1-309
A,Cross-references: GDB:118872; OMIM:182281
A,Map position: 17q12-17q12
C,Superfamily: macrophage inflammatory protein
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A; Status: preliminary
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C. Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 09-Jul-2004
C. Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 09-Jul-2004
C. Anderseion: A37236, A45817
R. Miller, M. D.; Wilson, S. D.; Dorf, M.E.; Seuanez, H.N.; O'Brien, S.J.; Krangel, M.S.
J. Immunol. 145, 2737-2744, 1990
A. Fitle: Sequence and chromosomal location of the 1-309 gene. Relationship to genes encotances number: A37236, MUID:91010756; PMID:2212659
A. Ference number: A37236, MUID:91010756; PMID:2212659
A. Accession: A37236
A. Accession: A37236
A. Cross-references: UNIPROT:P22362; GB:M57506; NID:9184505; PIDN:AAA52705.1; PID:9184506
R. Miller, M.D.; Hata, S.; Malefyt, R.D.W.; Krangel, M.S.
J. Immunol. 143, 2907-2916, 1989
A. Title: A novel polypeptide secreted by activated human T lymphocytes.
A. Reference number: A45817; MUID:90038522; PMID:2809212
A. Accession: A45817
A. Status: preliminary
A. Molecule type: mRNA
A. Residues: 1-96 cMIZA
A. Accession: A5817; MUID:90038522; PMID:AAA61196.1; PID:9339729
A. Cross-references: GB:M57502; NID:9339728; PIDN:AAA61196.1; PID:9339729
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C;Species: Cavia porcellus (guinea pig)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 148147
R;Yoshimura, T.
R;Yosh
C; Superfamily: macrophage inflammatory protein
C; Superfamily: macrophage inflammatory protein
C; Supervates: cytokine; glycoprotein; inflammation; pyroglutamic acid
E; 1-23/Domain: signal sequence #status predicted <SIG>
F; 24-99/Product: monocyte chemoattractant protein 1 #status experimental <MAT>
F; 29-99/Product: monocyte chemoattractant protein 1, short form #status experimental <MP
F; 24-99/Product: monocyte chemoattractant protein 1, short form #status experiment
F; 24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
F; 37/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Genetics: MCP-1
A;Gene: MCP-1
C;Superfamily: macrophage inflammatory protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 CCYTFNK-QIPLKRVKGYERITSSRCPQEAVIFRTLKNKEVCADPTQKWVQDYIAKLDQ 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYE-TNSQC
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                                                                                                                                                                                                                                                                                                                                                                                                                     25.2%; Score 127; DB 2; Length 99; 34.9%; Pred. No. 6.5e-07; ive 13; Mismatches 41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ::| | ::| | PKEAVIFKIVAKEICADPKQKWVQD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 SKPGIVFITKRGHSVCTNPSDKWVQD 85
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C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48093; JC2452; S30592; I49630
R;Heinrich, J.N.; Ryseck, R.P.; Macdonald-Bravo, H.; Bravo, R.
Myl. Cell. Biol. 13, 2020-2030, 1993
A;Title: The product of a novel growth factor-activated gene, fic, is a biologically acti
A;Reference number: A48093; MUID:93204948; PMID:8455595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: NIH 3T3 cells
R; Thirtion, S.; Nys, G.; Fiten, P.; Masure, S.; Damme, J.V.; Opdenakker, G.
Biochem. Biophys. Res. Commun. 201, 499-499, 1994
A; Title: Mouse macrophage derived monocyte chemotactic protein-3: cDNA cloning and identi
A; Reference number: JC2452; MUID:94271193; PMID:8002978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monocytic cytokine FIC - mouse
N;Alternate names: intercrine/chemokine; MARC/FIC protein; monocyte chemotactic protein-:
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A; Residues: 1-73,'A', 75-97 < THI>
A; Cross-references: GB:S71251; NID:9547088; PIDN:AAB30997.1; PID:9547089
A; Experimental source: LPS-stimulated WEHI-3 cells
R; Kulmburg, P.A.; Huber, N.E.; Scheer, B.J.; Wrann, M.; Baumruker, T.
A; Exp. Med. 176, 1773-1778, 1992
A; Title: Immunogloblin E plus antigen challenge induces a novel intercrine/chemokine in A; Reference number: S30592; MUID:93094785; PMID:1281219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-97 <HEI>
A;Cross_references: UNIPROT:Q03366; GB:L04694; NID:g192925; PIDN:AAA37516.1; PID:g192926
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                                                                                                                                                           1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYETNSQCS
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A;Residues: 1-73,'A',75-97 <KUL>
A;Cross-references: EMBL:Z12297; NID:g57937; PIDN:CAA78169.1; PID:g57938
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C;Keywords: glycoprotein
F;29/Binding site: carbohydrate (Asn) (covalent) #status predicted
        Length 96;
Query Match 24.4%; Score 123; DB 2; Length 96 Best Local Similarity 31.9%; Pred. No. 1.8e-06; Matches 29; Conservative 17; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.4%; Score 123; DB 2; 35.1%; Pred. No. 1.8e-06;
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                                                                                                                                                                                                                                                                                                                      61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMK 91
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C; Comment: It has not yet been shown that the previously detected eosinophilotactic pept;
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                 monocyte chemotactic protein bo-MCP-1b - bovine (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Species: J9-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-May-1997
C;Accession: A55984
R;Proost, P; Wuyts, A.; Lenaerts, J.P.; Van Damme, J.
Biochemistry 33, 13406-13412, 1994
A;Title: Purification, sequence analysis, and biological characterization of a second bc A;Reference number: A55984; MUID:95034774; PMID:7947749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-114 <MUE>
A;Cross-treferences: UNIPROT:P47992; EMBL:X86474; NID:g895846; PIDN:CAA60198.1; PID:g8958
R;Kennedy, J.; Kelner, G.S.; Kleyensteuber, S.; Schall, T.J.; Weiss, M.C.; Yssel, H.; Sc
J. Immunol. 155, 203-209, 1995
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A;Cross-references: GB:D43768; NID:g927650; PIDN:BAA07825.1; PID:g927651
A;Cross-references: GB:D43768; NID:g927650; PIDN:BAA07825.1; PID:g927651
C;Comment: Lymphotactin is produced by activated T-cells and is chemotactic for some lym C;Comment: Bosinophilotactic peptide is released from mast cells in lung and other tissu ially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N; Contrains: eosinophilotactic peptide
C;Species: Homo sapiens (man)
C;Date: 23-Oct-1981 #sequence revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: 860650; I38978; A03190; IS3506
R;Mueller, S.; Dorner, B.; Korthaeuer, U.; Mages, H.W.; D'Apuzzo, M.; Senger, G.; Krocze R;Mueller, S.; Jorner, B.; Rorthaeuer, U.; Mages, H.W.; D'Apuzzo, M.; Senger, G.; Krocze A;Title: Cloning of A7AC, an activation-induced, chemokine-related molecule exclusively
A;Reference number: 860650; MUID:95339892; PMID:7615002
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Proc. Natl. Acad. Sci. U.S.A. 72, 4123-4127, 1975
A;Title: Purification and synthesis of eosinophilotactic tetrapeptides of human lung tis
A;Reference number: A03190; MUID:76078412; PMID:1060093
A;Accession: A03190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N; Alternate names: activation-induced chemokine-related protein (ATAC); single cysteine
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A;Reference number: 138978; MUID:95325590; PMID:7602097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U23772; NID:g902001; PIDN:AAC50164.1; PID:g902002
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R;Yoshida, T.; Imai, T.; Kakizaki, M.; Nishimura, M.; Yoshie,
FEBS Lett. 360, 155-159, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 122; DB 2;
Pred. No. 1.7e-06;
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                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Moleoue type: protein
A:Residues: 1-72 <PRO>
C;Superfamily: macrophage inflammatory protein
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A; Residues: 1-114 < KEN>
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DKKN 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                         A Map position: 1923-1925

C'Superfamily: lymphotactin

C'Keywords: chemotaxis; cytokine; lymphokine; mast cell; T-cell

F.1-15/Domain: signal sequence #status predicted <SIG>

F.1-6-21/Domain: propeptide #status predicted <PRO>

F.22-114/Product: lymphotactin #status predicted <MAT>

F.22-25/Product: eosinophilotactic peptide #status predicted <MAT>

F.32-25/Product: eosinophilotactic peptide #status predicted <EOP>
                                                                                                                                                                                                                                                                                                                                                                                                     Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                 / Match 23.0%; Score 116; DB 1; Local Similarity 31.5%; Pred. No. 1.2e-05; les 29; Conservative 18; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 CSKPGIVFITKRGHSVCTNPSDKWVQDYIKDM 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 GSLRAVIFITKRGLKVCADPQATWVRDVVRSM
A, Gene: GDB:SCYCl; LIN; LPIN; ATAC
                                  A; Cross-references: GDB: 682094
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Adf15332 Human Adf16667 Human Adf16714 Human Adf16739 Human	5204 Human 5208 Human	3322	5712 Hun 5686 Hun 5694 Hun 1831 Mac	3172 Hun 2723 Hun 1138 Ant	2843 Hun 7600 Hun	3295 Ami 3020 Hun	107 HCC	641 640 640	5637 Hun 5634 Hun	5635 Hun 5635 Hun 5633 Hun	5639 Hun 5557 Hun 5554 Hun	1991 Hun	5553 Hun	5479 Hun 5545 Hun	5471 Hun 5470 Hun	5472 Hun	5594 Hun	7659 Ste	5589 Hun	5475 Hum 5473 Hum	5551 Hun 5474 Hun	853 HCC	549 Hun	595 Hun 1593 Hun	3943 NOV	552 Human 5565 Human	5591 Human	476 Human	5557 Human 5457 Novel	1994 H 1995 H 5559 H
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version 5.1.6 - 2005 Compugen Ltd.		6; Search time 165 Seconds (without alignments) 217.992 Million cell updates/sec	VCTNPSDKWVQDYIKDMKEN 93		residues	parameters: 2105692							results predicted by chance to have a to the score of the result being printed.	stribution.	SUMMARIES	Description		Hun	HA	HUH	Aab58994 Amino aci Aab50992 Human PRO	H	E E	Abu61834 Chemokine Abu61832 Human MTP	Pit	Human Human	Human	Human Human	213 Human 716 Human	Adf16713 Human alb Adf16715 Human alb Adf15205 Human alb

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AAR95691 standard; protein; 93 AA.
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100.0%; Pr
tive 0;
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                                                                                                                                                                                                                               (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                   Hawkins PR,
                                                                                                                                                                                                                                                                       WPI; 1996-277714/28
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Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                 N-PSDB; AAT31762
                                                                                                                                                                                                                                                                                                                of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 93 AA;
                                                                                                                          Homo sapiens.
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                                                                                                                                                                                      29-NOV-1995;
                                                                                                                                               WO9616979-A1
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                                                                                                                                                                  06-JUN-1996.
                                                   20-DEC-1996
                                                                                                                                                                                                                                                  Wilde CG,
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AAR95691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human macrophage inflammatory protein-1-gamma (MIP-1g) is used in therapeutic and diagnostic applications for detecting and treating infections, cancer, inflammation, myelopoietic dysfunction and autoimmune diseases. Antagonists/inhibitors of MIP-1g are used to treat diseases involving overexpression of MIP-1g, including silicosis, arteriosclerosis, autoimmune and chronic inflammatory and infective diseases, aplastic anaemia, etc. (Updated on 25-MAR-2003 to correct PN
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Add06562 Human Ckb
Adf14999 Human alb
                                                                                                                                                                                                                                                                                                                                                                                                                                          and -1 gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                       inflammatory protein-1-gamma; therapeutic; diagnostic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding human macrophage inflammatory proteins -3, -4 - used in immuno-regulation including inflammatory activity, haematopoiesis, treatment of psoriasis or solid tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 93;
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100.0%; Pred. No. 1e-52;
ive 0; Mismatches (
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                                          ALIGNMENTS
                                                                                                                                                                    Macrophage inflammatory protein-1-gamma.
                                                                                                                                                                                                                                                   /note= "signal peptide"
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 ADD06562
          ADF14999
                                                                                                                                                                                                                               Location/Qualifiers
                                                                                             AAR76128 standard; protein; 93 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 48; Fig 8; 60pp; English
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94US-00208339.
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 676
691
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Best Local Similarity
76.4
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                                                                                                                                                                                                                                                                                                                 28-JUN-1994;
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02-DEC-1995
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                                                                                                                                                                                       Macrophage
                                                                                                               AAR76128;
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                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leukocyte; attractant; affinity; leukaemia; immunity; wound healing; diagnosis; drug screening; inflammation; haematopoidesis regulator; pporiasis; stroke; thrombocytosis; pulmonary embolism; asthma; arthritis; aplastic anaemia; endotoxic shock; MIP; macrophage inflammatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liver and pituitary gland expressed chemokine(s) - useful for diagnosis
                                              Chemokine, liver, pituitary gland, LVBC; PGEC; inflammation, detection; identification, MCP receptor, CC-CKRI receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYETNSQCS
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                                                                                                                                                                                                                                                                                                                                                                                                                       Seilhamer JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 504; DB 2; ]
Pred. No. 1e-52;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human MIP-4: a chemoattractant for leukocytes.
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Pituitary expressed chemokine (PGEC)
                                                                                                                                                                                                                                                                                                                                                                                                                       Bandman O,
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Human M-CIF protein.
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                                                                                                                                                        (FORS/) FORSSMANN W.
                                                                                                                                                                                                               N-PSDB; AAT95743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 93 AA;
                                                                                                                                  30-APR-1996;
                                                                                                             30-APR-1997;
                                            ношо варіепв
                                                                WO9741230-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-0CT-1998
                                                                                      16-NOV-1997
                                                                                                                                                                                                                                                            functions
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                                                                                                                                                                                                                                                                                                                        Human macrophage inflammatory protein-4 (MIP-4) is an attractant for leucocytes and is involved in the regulation of immune responses and inflammation, e.g. stimulating synthesis of other cytokines. DNA encoding MIP-4, MIP-4, MIP-4, and agonists of MIP-4 are useful for protecting bone marrow against chemotherapeutic agents, for eliminating leukaemia cells (by inducing apoptosis), stimulating an immune response and regulating inducing apoptosis), stimulating proliferation and differentiation of cells) and lymphocyte trafficking. MIP-4 is also used to treat psoriasis and solifertion and to stimulate wound healing. MIP-4 also increase vascular permeability, and can be used to treat stroke, thromobocytosis, pulmonary embolism and myeloproliferative disease, and for identification of specific receptors. Antagonists of MIP-4 are used to inhibit the production of II-1 and TNP-alpha and to treat e.g. aplastic anaemia, myelodysplastic syndrome, asthma, arthritis (and many other autoimmune and inflammatory diseases), infections, endotoxic shock, atherosclerosis, allergy etc. MIP-4 and DNA encoding it may also be used in drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                              New nucleic acid encoding the new human chemokine beta-8 - with chemo:attractant activity for leucocytes, for treating leukaemia, stimulating immunity and wound healing, also for diagnosis and drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 504; DB 2
Pred. No. 1e-52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                        H, Adams MD;
                     1. .19
/label= sig_peptide
                                          20. .93
/label= mat_protein
          Location/Qualifiers
                                                                                                                                                                                                                                                                                                       Example 2; Page 58; 93pp; English.
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                                                                                                                                                                                        Ruben SM,
                                                                                                                                                                                                              WPI; 1996-506106/50.
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                                                                            WO9634891-A1
                                                                                                                      23-JUN-1995;
                                                                                                                                            05-MAY-1995;
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                     Peptide
                                            Protein
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Novel nucleic acids of a tandem gene contain AAT95743 or AAT95744 and encode the human chemokines CC-2 and CC-3. Transcription of the tandem gene generates a biciatronic mature RNA containing two non-overlapping open reading frames (ORF). AAT95743 has a 1st ORF for AAW38170, i.e. CC-2, and a 2nd ORF for AAW38171, i.e. the known chemokine HCC-1. AAT95744, formed by alternative splicing of the primary transcript, has the same ist ORF but the 2nd encodes AAW38172, a variant form of HCC-1 having a 16 amino acid insertion, i.e. CC-3. The tandem gene has two functional promoter regions, suggesting independent expression of the ORF. cDNA for the bicistron was produced from the total RNA of T84 cells by 5'-rapid maplification of complementary ends (RAC1). The gene corresponding to this DNA was isolated on chromosome 17, and found to have seven exons, four for CC-2 and three for HCC-1/CC-3, separated by about 12 kb. CC-2 and CC-3 can be used to treat disorders of cell migration, the immune system and growth functions. Also antibodies against them, and fragments that hybridise to the CDNA, can be used for diagnosis. (Updated on 25-MAR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid of tandem human gene for chemokines CC-2 and CC-3 - us for treating disorders of cell migration, the immune system and growth
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Tandem gene; chemokine CC-2; chemokine CC-3; chemokine HCC-1; human; cell migration; immune system.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 504; DB 2; Length 93; 100.0%; Pred. No. 1e-52; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maegert H, Schulz-Knappe P;
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                                                                                                                                                                                                                                                                                                                                                                                      97WO-EP002217.
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Best Local Similarity 100.0
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The present invention relates to methods for stimulating or inhibiting angiogenesis and cardiovascularization. The methods involve the use of pharmaceutical compositions based on the following proteins, PRO179, PRO286, PRO344, PRO846, PRO1760, PRO256, PRO321, PRO331, PRO840, PRO877, PRO877, PRO879, PRO879, PRO879, PRO877, PRO879, CALGORIAN WERE DESCRIPTION OF THE PROFILE OF THE PROSPECT OF THE PROSPECT OF THE PROFILE OF THE PROFILE OF THE PROSPECT OF THE PROFILE OF THE OF THE OF THE OF THE OF THE OF THE PROFILE OF THE OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel PRO polypeptides and agonists and antagonists of them, used to diagnose and treat cardiovascular, endothelial and angiogenic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen ME;
Paoni NF, Pitti RM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baker KP, Ferrara N, Gerber H, C
rney AL, Hillan KJ, Marsters SA,
Milliams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
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                             1. .22
/label= Signal peptide
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Location/Qualifiers
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                                                                                                                                                                                                                                                                              99WO-US005028.
99WG-US12557.
99WG-US01255.
99WG-U45688.
99WG-U302111.
99WG-US02111.
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Goddard A, Gurney AL, Hil
Watanabe CK, Williams PM,
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05-JAN-2000;
18-FEB-2000;
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                                                                                                                                                                       14-SEP-2000
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                             Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a monocyte colony inhibitory factor (M-CIF) which is used in a method for inhibiting proliferation or differentiation of myeloid progenitor cells, specifically low proliferative potential colony forming cells or colony forming unit-granulocyte and monocyte and monocyte or cells, in an human individual undergoing therapy that kills dividing cells, especially chemotherapy or radiation therapy, where the polypeptide results in accelerated recovery of platelets or granulocytes alleviating thrombocytopaenia or neutropaenia. The polypeptide can be administered to treat a myeloproliferative disorder, especially essential thromobycytosis, polycythemia vera and agnogenic myeloid metaplasia. The polypeptide can also be used for myeloprotection, to inhibit growth of paramatopojetic progenitor cells, to treat sepsis, to suppress TNF-alpha production, to treat renal injury, arthritis or joint inflammation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting proliferation or differentiation of myeloid progenitor cells using myeloid progenitor inhibitory factor-1 amino-terminal deletion mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                             Antonaccio M, Mendrick D;
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  myeloproliferative disorder; suppressor; inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Patel V,
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                                                             Homo sapiens
                                                                                                                  WO9814582-A1
                                                                                                                                                                                                                               10-SEP-1997;
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                                                                                                                                                                          09-APR-1998
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Jimenez P;
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Gaps ó; 9

AAB27659 RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide 3, amide and heterocyclic compounds and saccharide conjugates used for inhibiting chemokine induced activity and for treating e.g. stroke, vascular diseases, autoimmune diseases and tumor growth.
                              monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV; AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia; basophil-mediated disease; myocardial infarction; acute ischaemia; rhenmatoid arthritis; contraception.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention concerns the identification of a number of chemokines which can be used to produce derivatives, agonists and antagonists which are then useful in disease treatment. The chemokines include sequences ABBIS785-BIS794, ABBIS003-BIS813 and AABIS813-BIS848. These chemokine derivatives can be used to treat diseases such as autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated diseases, endotoxaemia, myocardial infarction, acute ischaemia and theumatoid arthritis, and can be used to prevent strokes and as contraceptives. The coding sequences for the chemokines can be used in gene therapy for the same diseases, as well as in the production of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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Pred. No. 1e-52;
; Mismatches 0; Indels
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99US-00271192.
99US-00452406.
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93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       animal models
                                                                                                                  Homo sapiens
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Best Local S
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The present sequence represents a fragment of an untruncated human chemokine PHC-1. Peptides derived from truncated PHC-1 are inhibitors of chemokine receptors, especially the CCR5 receptor. Processed PHC-1 chemokines are useful for prevention and treatment of a disease induced by viral infections, a bacterial agent or a protozoa. They are also conseful for prevention and/or the treatment of a disease induced by viral infections, cancers, restencisis, allergies, allergies, psoriasis, chronic contact dermatitis, inflammatory bowel disease, multiple chronic contact dermatitis, inflammatory bowel disease, multiple contact dermating pain, diabetes, obsetty, anorexia, bulimia, induced by pathogeneous agent. They are also useful for wound and bone contact disease, acute heart failure, hypotension, hypertension, curinary retention, osteoporosis, angina pectoris, myocardial infarction, ischemia, ulcers, migraine, vomiting, psychotic and neurological construction, merchanical and severe mental retardation, degenerative diseases, and dyskinesias concurs and neurolegenerative diseases such as Alzheimer's disease, and dyskinesias concurs and neurological neurodegenerative diseases such as Alzheimer's disease, and dyskinesias concurs and severe mental retardation, degenerative diseases such as Huntington's disease or Gilles de la Tourette's syndrome
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multiple sclerosis; organ transplant rejection; infection; wound healing; bobe healing; pain; diabetes; obsely; anorexia; bulinia; osteoporosis; Parkinson's disease; acute heart failure; hypotension; hypotension; urinary retention; angina pectoris; myocardial infarction; ischemia; unioer; migraine; vomiting; psychotic disorder; neurological disorder; anxiety; schizophrenia; depression; delirium; dementia; dyskinesia; mental retardation; degenerative disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multiple sclerosis, stroke, sarcoidosis or organ transplant rejection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           processed human chemokines or their derivatives useful for preven
treating viral infections, inflammation, cancer, atherosclerosis,
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                                                                                                                                                 Alzheimer's disease; Huntington's disease; Gilles de la Tourette's syndrome.
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22-JUN-2000; 2000EP-00870140.
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108 93; Conservative
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KIRCHHOFF F
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Pred. No. 1e-52;

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61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93 61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN

93

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Best Local Similarity
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                                         Human, PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive; vasotropic, antirheumatic; antiarthritic; antiinflammatory; cytostatic; vulnerary; antianginal; gene therapy; cardiovascular disease; endothelial disorder; angiogenic disorder; cancer; periodontal disease;
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PJ, Gurney AL, Kuo SS, Mark MR, M
Watanabe CK, Williams PM, Wood WI;
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Goddard A, Godowski PJ, Gurney AL,
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05-JAN-2000; 2000W0-US000319.

06-JAN-2000; 2000W0-US000376.

11-FEB-2000; 2000W0-US00341.

18-FEB-2000; 2000W0-US004342.

24-FEB-2000; 2000W0-US004342.

24-FEB-2000; 2000W0-US005841.

02-MAR-2000; 2000W0-US005841.
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99US-0141037P.
99US-0144758P.
99US-0145698P.
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99WO-US028409.
99WO-US028565.
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21-MAR-2000; 2000WO-US007532
                                                                                                                            2000WO-US013705
             (first entry)
                                        PRO; cardiant;
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                          Human PRO877 protein.
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Paoni NF, Pitti RM,
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                                                                                                 WO200073445-A2
                                                                     wound healing
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28-JUL-1999;
01-SEP-1999;
30-NOV-1999;
30-NOV-1999;
02-DEC-1999;
                                                                                   Homo sapiens
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             21-MAR-2001
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AAB50992;
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Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; immunostimulant; antiangiogeneis; tumour; necanglogeneis; sascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;

Human Tumour Endothelial Marker polypeptide SEQ ID NO 279

(first entry)

30-MAY-2002

ABB90773;

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ABB90773 standard; protein; 93

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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a ABB90749, ABB90750 and ABB90760. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, necangiogenesis in subjects bearing a vascularised tumour, polycystic kiney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABB90755-ABB92078-ABB92191 and ABB90721-ABB90789) are disclosed, as are marker oligonuclectide sequences: tumour endothelial markers (NEM) ABL92041-ABB92041, and pan-endothelial markers (NEM) ABL92042, and pan-endothelial markers
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An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
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100.0%; Pred. No. 1e-52;
ive 0; Mismatches 0;
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Best Local Similarity
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Matches
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The present sequence is one of seventeen novel PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating periodontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or angiogenic disorder

DB 4; Length 93;

100.0%; Score 504;

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Sequence 93

Query Match

Seventeen nucleic acids encoding PRO polypeptides which are useful ir diagnosis and treatment of cardiovascular, endothelial or angiogenic

Claim 71; Fig 28; 182pp; English.

in a mammal.

disorders

Kinzler KW, Vogelstein B;

St Croix B,

WPI; 2002-291856/33. N-PSDB; ABL92128.

(UYJO) UNIV JOHNS HOPKINS

02-AUG-2000; 2000US-0222599P. 11-AUG-2000; 2000US-0224360P

01-AUG-2001; 2001WO-US024031

WO200210217-A2 Homo sapiens.

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07-FEB-2002

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Human, mouse, rat, TEM, tumour endothelial marker, NEM, PEM, cytostatic, normal endothelial marker; pan-endothelial marker, immunostimulant, antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
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11-APR-2001; 2001US-0282850P.
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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a ABB90719, and ABB90715. ABB90710, ABB90719, ABB90719, ABB90710, ABB90719, ABB90719, ABB90710, ABB90719, ABB90710, They are useful for inhibiting tumour growth, necangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABB90705-ABB92114 and ABB90711-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL92041 and ABB90711-ABB90719, normal endothelial markers (NEM) ABL92041, and pan-endothelial markers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; immunostimulant; antiangiogenic; tumour; necangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
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                                KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN
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11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-2002
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Similarity

Query Match Local Matches 9

MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS 60

1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS

100.0%; Score 504; DB 5; Length 93; 100.0%; Pred. No. 1e-52;

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The invention relates to a novel chemokine, de-ubiquitination or cell surface protein. The composition is useful for modulating physiology or development of a cell or tissue culture cells. The present sequence represents the amino acid sequence of human MIP-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising HCC5, Dubl1, Dubl2, primate MD1 or MD2 or rodent MD2 polypeptide, useful for modulating physiology or development of a cell or tissue culture cells.
                                                                                                                                                                                          New composition comprising HCC5, Dubl1, Dubl2, primate MD1 or MD2 or rodent MD2 polypeptide, useful for modulating physiology or development of a cell or tissue culture cells.
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                                99US-00372348
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tissue culture development
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Best Local Similarity
                                                                                             (BAZA/) BAZAN J F.
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                                                                12-AUG-1998;
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                                11-AUG-1999;
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06-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel chemokine, de-ubiquitination or cell surface protein. The composition is useful for modulating physiology or development of a cell or tissue culture cells. The present sequence represents the amino acid sequence of chemokine HCC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         " composition comprising HCC5, Dubl1, Dubl2, primate MD1 or MD2 or dent MD2 polypeptide, useful for modulating physiology or development a cell or tissue culture cells.
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                                                                                                                                                                                                                Chemokine; HCC1; cell development; tissue culture development.
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 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
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                                                                                ABU61834 standard; protein; 93 AA
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Best Local Similarity
Best Local 93; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal endothelial marker (TEM), normal endothelial marker (DEM), and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neongiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. The present
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The invention relates to a novel chemokine, de-ubiquitination or cell surface protein. The composition is useful for modulating physiology or development of a cell or tissue culture cells. The present sequence represents the amino acid sequence of the pituitary expressed chemokine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endothelial cell; EC; tumour endothelial cell; TEM; NEM;
                                                                                                                                                                 6; Length 93;
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                                                                                                                                                            100.0%; Score 504; DB 6; 100.0%; Pred. No. 1e-52; ive 0; Mismatches 0
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06-FEB-2002; 2002US-0354262P.
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Best Local Similarity
---- 93; Conserve
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                                                                                                                   Sequence 93 AA;
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ABUS4479
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ABUS479
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Human KW Tumoun
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sequence represents a human TEM or NEM protein of the invention
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                                                                                                                        100.0%;
100.0%;
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06-FEB-2002; 2002US-0354262P
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Best Local Similarity 100.
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N-PSDB; ABX72054.
                                                             Sequence 93 AA;
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Gaps

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Indels

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Matches

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0; Mismatches
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                                                                                                                                                                                                                        ABP76018 standard; protein;
                                                                                                                                                                                                                                                                                         (first entry)
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 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tanaka H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-075548/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200283898-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
                                                                                                                                                                                                                                                                                         21-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                          ABP76018;
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Matches
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 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal polynucleottelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleottel sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour andiogenesis, for for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
                                                                                                           1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour anglogenesis; neoangiogenesis; immune response; cytostatic; antidiabetic, ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
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                   Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinzler KW, Vogelstein B;
                 100.0%; Score 504; DB 6; 100.0%; Pred. No. 1e-52;
                                                                                                                                                       93
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                                                                                                                                                                          KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN
                                                   0; Mismatches
                                                                                                                                                       KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN
                                                                                                                                                                                                                                                                                                                                                                              Human normal endothelial marker NEM 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 316; 374pp; English.
                                                                                                                                                                                                                                                                           ABU54480 standard; protein; 93
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100.0%;
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06-FBB-2002; 2002US-0354262P.
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                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-093016/08.
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Best Local Similarity
                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABX72053
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                                                 93;
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                     Query Match
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ABU54480

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
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                                                               1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYETNSQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metal toxicity, cancer, inflammatory diseases, immune disorders, and t
neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
1 MKISVAAIPPFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer;
inflammatory disease; immune disorder; neuromuscular; toxicity;
central nervous system; cardiovascular; gastrointestinal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; nootropic; neuroprotective; cardiant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
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                                                                                                                                              KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
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                                                                                                                                                                                                                                                                                                                                                                                                     93
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The present invention describes a human chemokine betal (Ckbl) protein (I) comprising a deletion in amino acid residues from the amino terminus and/or carboxy terminus of the 31 residue amino acid sequence (S1, see and/or carboxy terminus of the 32 residue amino acid sequence (S1, see ADD06466). (I) has anti-HIV, neuroprotective, antithyroid, antiarthritic, antiathematic, immunosuppressive, nootropic, antiathyroid, antiarthritic, cantiarthematic, antiathlergic, osteopathic, nephrotrophic, tuberculostatic, virucide, antiatherosclerotic and antimicrobial activities. (I) is useful for preventing infection, preferably viral (human immunodeficiency virus (HIV)) infection, in a cell, by contacting the cell with (I). (I) is also useful for treating a disease, such as HIV infection or immune disorders, haematopoietic disorders, autoimmune disorders, multiple sclerosis, Grave's disease, arthritis, rheumatoid arthritis, transplant rejection, neurodegenerative disorders, inflammatory bowel disease, inflammatory disease, inflammatory disease, colitis, inflammatory bidney diseases, glomerulonephritis, infection, or individual. (I) inhibits or abolishes the ability of HIV to bind to, colitis, into/fuse with (infect), and/or replicate in CCRS expressing cells, inhibit CRS ligand binding to a CRS molecule, or upregulate or downrequlate CRS expression. (I) also acts a CRS agonists or antegonists, stimulate chemotaxis of commendate or downrequlate or downrequlate or downrequlate or downrequlate or downrequlate or downrequlate or differential indentification of the tissues or immunological probe for the differential identification of the tissues or immunological probe for the differential dientification of the tissues or immunological probe for the differential identification of the tissues or immunological probe for the differential identification of the tissues or immunological probe for the differential identification of the tissues or diagnosing, treating and preventing various disorders in mammals,
                                                                                                                                                                                                                                                                                                                                                          antiarthritic, antirheumatic; antialergic osteopathic; antiarthritic; antiarthrit
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                                                                                                                                                                                                                                                                                                                                   chemokine betal; Ckbl; anti-HIV; neuroprotective; antithyroid;
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                                         ADD06466 standard; protein; 93 AA
                                                                                                                                                                                                                                                           Human Ckbl protein SEQ ID NO:2.
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                                                                                                                                                                                  (first entry)
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                                                                                                              ADD06466;
ADD06466
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preferably in humans. (I)-HSA fusion proteins are also useful as molecular weight markers on sodium dodecyl sulfate polyacrylandade gel electrophoresis techniques, for raising antibodies, and to test the biological activities of the Ckbl protein. (I)-HSA fusion proteins are useful for screening for molecules that bind to the Ckbl protein portion of the fusion protein. The present sequence represents human Ckbl, which is used in the exemplification of the present invention.
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                                                                                                                                                                              1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYETNSQCS
                                                                                                                                                                                                    1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    albumin fusion protein; albumin activity; human serum albumin; serum osmotic pressure; shelf-life; stability; antidiabetic; gene therapy; diabetes mellitus; human; gene; ds.
                                                                                                                            DB 7; Length 93;
                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                             Human albumin fusion protein-related protein SeqID511.
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                                                                                                                           100.0%; Score 504; DB 7; 100.0%; Pred. No. 1e-52; ive 0; Mismatches 0;
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DELTA BIOTECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                   ADF15213 standard; protein; 93
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2002US-0370227P.
2002US-0378950P.
2002US-0382617P.
2002US-0383123P.
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2002US-0402131P.
2002US-0402708P.
2002US-0411355P.
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2002US-0350358P.
2002US-0351360P.
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2002US-0360000P
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                                                                                                                           Query Match
Best Local Similarity 100.'
Matches 93; Conservative
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                                                                                                    Sequence 93 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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08-APR-2002;
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24-MAY-2002;
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                                                                                                                                                                                                                                                                                            RESULT 21
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2002US-0402708P.
2002US-0411355P.
                                                                                                                                                                                                                                   treating diabetes mellitus.
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                                                                                                                                                            Ballance DJ, Turner AJ,
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Matches 93; Conservative
                                                                                                                                                                                   WPI; 2003-598517/56.
                                                                                                                                                                                                 N-PSDB; ADF16390.
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                                  18-SEP-2002; 2
02-OCT-2002; 2
11-OCT-2002; 2
23-OCT-2002; 2
                                                                                    05-NOV-2002;
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(PRIN-) 1
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                                                                                          This invention relates to a novel albumin fusion protein having albumin or biological activity. Human serum albumin is responsible for a Significant proportion of the osmotic pressure of serum and also functions as a carrier of endogenous and exogenous ligands. The fusion of albumin to a therapeutic protein may increase shelf-life and stability of allow production of compositions with antidiabetic activity whilst the nucleotide sequence which encodes it may be useful for gene therapy. The albumin fusion protein is useful for preparing a composition for treating diabetes mellitus. The present sequence is that of a therapeutic protein which was fused with human albumin to create a novel albumin fusion protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                        1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
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                             New albumin fusion protein, useful for preparing a composition for treating diabetes mellitus.
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                                                                                                                                                                                                                                                                                                          100.0%; Score 504; DB 7; 100.0%; Pred. No. 1e-52;
                                                                                                                                                                                                                                                                                                                                                                                                          61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93
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                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                      Example 4; SEQ ID NO 511; 24pp; English.
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10-MAY-2002; 2002US-03378950P.
24-MAY-2002; 2002US-0383123P.
28-MAY-2002; 2002US-0383123P.
05-JUL-2002; 2002US-0385708P.
10-JUL-2002; 2002US-0394625P.
24-JUL-2002; 2002US-03980008P.
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2002US-0351360P.
2002US-0359370P.
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                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
Hes 93; Conservative
WPI; 2003-598517/56.
N-PSDB; ADF15778.
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26-FEB-2002;
28-FEB-2002;
27-MAR-2002;
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This invention relates to a novel albumin fusion protein having albumin or biological activity. Human serum albumin is responsible for a significant proportion of the osmotic pressure of serum and also functions as a carrier of endogenous and exogenous ligands. The fusion of albumin to a therapeutic protein may increase shelf-life and stability of the therapeutic protein. The albumin fusion protein of the invention may allow production of compositions with antidiabetic activity whilst the nucleotide sequence which encodes it may be useful for gene therapy. The albumin fusion protein is useful for preparing a composition for treating diabetes mellitus. The present sequence is that of a therapeutic protein which was fused with human albumin to create a novel albumin fusion protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpot_sequences
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                                   2002US-0414984P.
2002US-0417611P.
2002US-0420246P.
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PRINCIPIA PHARM CORP.
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2002US-0411426P
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albumin fusion protein; albumin activity; human serum albumin; serum osmotic pressure; shelf-life; stability; antidiabetic; gene therapy; diabetes mellitus; human; gene; ds.
                                 Human albumin fusion protein-related protein SegID1817.
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                                                                                                     Homo sapiens
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28-JAN-2002;
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 or biological activity. Human serum albumin is responsible for a significant proportion of the osmotic pressure of serum and also functions as a carrier of endogenous and exogenous ligands. The fusion of albumin to a therapeutic protein may increase shelf-life and stability of the therapeutic protein may increase shelf-life and stability of the therapeutic protein. The albumin fusion protein of the invention may allow production of compositions with antidiabetic activity whilst the nucleotide sequence which encodes it may be useful for gene therapy. The albumin fusion protein is useful for preparing a composition for treating diabetes mellitus. The present sequence is that of a therapeutic protein which was fused with human albumin to create a novel albumin fusion protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/publishedpct_sequences
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treating diabetes mellitus.
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                                                                  2002US-0360000P.
2002US-0367500P.
2002US-0370227P.
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2002US-0411426P.
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                                                       2002US-0359370P
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2002WO-US040891
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Query Match
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                                                                                                   10-MAY-2002;
24-MAY-2002;
28-MAY-2002;
23-DEC-2002;
                                                                             27-MAR-2002;
08-APR-2002;
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09-AUG-2002;
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2002US-0359370P. 2002US-0360000P. 2002US-0367500P. 2002US-0370227P.

2002US-0382617P 2002US-0383123P 2002US-0385708P 2002US-0398008P. 2002US-0402708P.

2002US-0394625P

2002US-0378950P

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This invention relates to a novel albumin fusion protein having albumin or biological activity. Human serum albumin is responsible for a functionat proportion of the osmotic pressure of serum and also functions as a carrier of endogenous and exogenous ligands. The fusion of albumin to a therapeutic protein may increase shelf-life and stability of the therapeutic protein. The albumin fusion protein of the invention may allow production of compositions with antidiabetic activity whilst the nucleotide sequence which encodes it may be useful for gene therapy. The albumin fusion protein is useful for preparing a composition for treating diabetes mellitus. The present sequence is a that of a therapeutic protein which was fused with human albumin to create a novel albumin fusion protein of the invention. Note: The sequence data for this patent did not
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Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
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                                                                                  WPI; 2003-598517/56.
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61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93 61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN

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ઠે a ADF16715 standard; protein; 93 AA

RESULT 24 ADF16715 ID ADF1 XX AC ADF1

ADF16715

1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS

DELTA BIOTECHNOLOGY LTD. PRINCIPIA PHARM CORP.

HUMAN GENOME SCI INC.

2002US-0414984P

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allow production of compositions with antidiabetic activity whilst the mucleotide sequence which encodes it may be useful for gene therapy. The albumin fusion protein is useful for preparing a composition for treating diabetes mellitus. The present sequence is that of a therapeutic protein which was fused with human albumin to create a novel albumin fusion protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
the therapeutic protein. The albumin fusion protein of the invention may
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DELTA BIOTECHNOLOGY LTD.
PRINCIPIA PHARM CORP.
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2002US-035338P.
2002US-0353370P.
2002US-035370P.
2002US-0376220P.
2002US-0376220P.
2002US-0376220P.
2002US-037856P.
2002US-037856P.
2002US-038123P.
2002US-0385708P.
2002US-0385708P.
2002US-0396008P.
2002US-040208P.
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28-FEB-2002;
27-MAR-2002;
08-APR-2002;
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24-MAY-2002;
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(DELZ )
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                                           MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYETNSOCS
                     MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
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                                                                                                                   KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN
                                                                                               KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-DEC-2001; 2001US-0341811P.
24-JAN-2002; 2002US-0350358P.
26-FBB-2002; 2002US-0351360P.
28-FBB-2002; 2002US-0359370P.
28-FBB-2002; 2002US-0367500P.
28-ARAY-2002; 2002US-0367500P.
10-MAY-2002; 2002US-037622P.
10-MAY-2002; 2002US-0378251P.
28-MAY-2002; 2002US-038570P.
28-MAY-2002; 2002US-0411355P.
28-MAY-2002; 2002US-0411426P.
28-CCT-2002; 2002US-0411426P.
                                                                                                                                                                                                                                ADF15205 standard; protein; 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-2002; 2002US-0420246P. 05-NOV-2002; 2002US-0423623P.
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                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                          12-FEB-2004
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                                                                                               61
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ADF15205
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(DELZ
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                                                                                                             This invention relates to a novel albumin fusion protein having albumin or biological activity. Human serum albumin is responsible for a significant proportion of the osmotic pressure of serum and also functions as a carrier of endogenous and exogenous ligands. The fusion of albumin to a therapeutic protein may increase shelf-life and stability of the therapeutic protein may increase shelf-life and stability of allow production of compositions with antidiabetic activity whilst the nucleotide sequence which encodes it may be useful for gene therapy. The albumin fusion protein is useful for preparing a composition for treating diabetes mellitus. The present sequence is that of a therapeutic protein which was fused with human albumin to create a novel albumin fusion protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpot_sequences
                                                                                                                                                                                                                                                                                                                                                           1 MKISVAAIPPFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS 60
                                                                                                                                                                                                                                                                                                                                                                        MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS 60
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                       New albumin fusion protein, useful for preparing a composition for
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               albumin fusion protein; albumin activity; human serum albumin; serum osmotic pressure; shelf-life; stability; antidiabetic; gene therapy; diabetes mellitus; human; gene; ds.
                                                                                                                                                                                                                                                                                                              100.0%; Score 504; DB 7; Length 93; 100.0%; Pred. No. 1e-52;
                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human albumin fusion protein-related protein SegID1769
Rosen CA, Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                                                                         93
                                                                                                                                                                                                                                                                                                                                                                                                         61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN
                                                                                                                                                                                                                                                                                                                                                                                                                    KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                        Example 4; SEQ ID NO 631; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADF16667 standard; protein; 93 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002US-035035BP.
2002US-0351360P.
2002US-0359370P.
2002US-0360000P.
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2002US-0370227P.
2002US-0378950P.
2002US-0382617P.
2002US-0383123P.
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                                                                 treating diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                    93; Conservative
Turner AJ,
                      WPI; 2003-598517/56
                                                                                                                                                                                                                                                                                                                        Local Similarity
                                  N-PSDB; ADF15897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003060071-A2
                                                                                                                                                                                                                                                                                        Sequence 93 AA;
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28-MAY-2002; 2
05-JUN-2002; 2
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08-APR-2002; 2
10-MAY-2002; 2
Ballance DJ,
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28-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-2002;
28-FEB-2002;
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This invention relates to a novel albumin fusion protein having albumin or biological activity. Human serum albumin is responsible for a significant proportion of the osmotic pressure of serum and also functions as a carrier of endosnous and exogenous ligands. The fusion of albumin to a therapeutic protein may increase shelf-life and stability of the therapeutic protein may increase shelf-life and stability of allow production of compositions with antidiabetic activity whilst the nucleotide sequence which encodes it may be useful for gene therapy. The albumin fusion protein is useful for preparing a composition for treating diabetes mellitus. The present sequence is that of a therapeutic protein which was fused with human albumin to create a novel albumin fusion protein of the invention. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRORIMDYYETNSQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New albumin fusion protein, useful for preparing a composition for treating diabetes mellitus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 504; DB 7; Length 93; 100.0%; Pred. No. 1e-52; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   Haseltine WA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO 1769; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Turner AJ, Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADF16714 standard; protein; 93 AA
                                                                                                                                                                                                                                                                      HUMAN GENOME SCI INC.
DELTA BIOTECHNOLOGY LTD.
PRINCIPIA PHARM CORP.
2002US-0402131P.
                                                                                                                                                2002US-0417611P.
                                                         2002US-0411355P.
2002US-0411426P.
                                                                                                                         2002US-0414984P
                                                                                                                                                                                                                2002US-0423623P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-598517/56.
N-PSDB; ADF16341.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                   02-OCT-2002;
11-OCT-2002;
23-OCT-2002;
                                13-AUG-2002;
                                                         18-SEP-2002;
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09-AUG-2002;
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albumin fusion protein; albumin activity; human serum albumin; serum osmotic pressure; shelf-life; stability; antidiabetic; gene therapy; diabetes mellitus; human; gene; ds.
                                                      Human albumin fusion protein-related protein SegID1841.
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                                                                                                                                                                                            23-DEC-2002; 2002WO-US040891
                                                                                                                                                WO2003060071-A2
                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                        28-MAY-2002;
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02-OCT-2002;
                                                                                                                                                                                                                                         28-JAN-2002;
                                 12-FEB-2004
                                                                                                                                                                       24-JUL-2003
          ADF16739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIN-)
This invention relates to a novel albumin fusion protein having albumin or biological activity. Human serum albumin is responsible for a significant proportion of the osmotic pressure of serum and also functions as a carrier of endogenous and exogenous ligands. The fusion of albumin to a therapeutic protein may increase shelf-life and stability of the therapeutic protein. The albumin fusion protein of the invention may albumin fusion protein of the invention may albumin fusion protein is useful for preparing a composition for treating diabetes mellitus. The present sequence is that of a therapeutic protein protein was fused with human albumin to create a novel albumin fusion protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                   New albumin fusion protein, useful for preparing a composition for treating diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 504; DB 7; Length 93; 100.0%; Pred. No. 1e-52;
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Pred. No. 1e-52;
                                                                                                                                                                                                                                                                                                                                               Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
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                                                                                                                                                                                                                                                                                                  HUMAN GENOME SCI INC.
DELTA BIOTECHNOLOGY LTD.
                                                                        26-FEB-2002; 2002US-03593700.
28-FEB-2002; 2002US-0369000P.
27-MAR-2002; 2002US-0367500P.
08-APR-2002; 2002US-0370227P.
10-MAY-2002; 2002US-0378950P.
28-MAY-2002; 2002US-038123P.
05-JUN-2002; 2002US-0381328P.
                                                                                                                                                                                                                                                                                                                        PRINCIPIA PHARM CORP.
                                                                                                                                                                     10-JUL-2002, 2002US-0394625P.
24-JUL-2002, 2002US-0398008P.
09-AUG-2002, 2002US-0402131P.
13-AUG-2002, 2002US-0402708P.
                                                                                                                                                                                                                   18-SEP-2002; 2002US-0411355P.
18-SEP-2002; 2002US-0411426P.
02-OCT-2002; 2002US-0414984P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 93 AA;
                                                                                                                                                                                                                                                     11-OCT-2002;
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(PRIN-)
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2002US - 0370227P 2002US - 0378950P 2002US - 0383123P 2002US - 0387028P 2002US - 0394625P 2002US - 0396008P

2002US-0359370P. 2002US-0360000P. 2002US-0367500P.

2002US-0402131P. 2002US-0402708P. 2002US-0411355P.

2002US-0411426P. 2002US-0414984P. 2002US-0417611P. 2002US-0420246P.

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This invention relates to a novel albumin fusion protein having albumin or biological activity. Human serum albumin is responsible for a significant proportion of the osmotic pressure of serum and also functions as a carrier of endogenous and exogenous ligands. The fusion of albumin to a therapeutic protein may increase shelf-life and stability of albumin to a composition with antidiabetic activity whilst the nucleotide sequence which encodes it may be useful for gene therapy. The albumin fusion protein is useful for preparing a composition for treating diabetes mallitus. The present sequence is that of a therapeutic protein which was fused with human albumin to create a novel albumin fusion protein in growein to the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ffp.wipo.int/pub/publishedpct_sequences
                                                                                                                                         New albumin fusion protein, useful for preparing a composition for treating diabetes mellitus.
                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO 1841; 24pp; English.
WPI; 2003-598517/56.
                                                      N-PSDB; ADF16413
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0; Mismatches

93; Conservative

Matches

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1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS 1 MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS

61 KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN 93

ADF16739 standard; protein; 93 AA.

RESULT 29 ADF16739 ID ADF16

Haseltine WA;

DELTA BIOTECHNOLOGY LTD.

HUMAN GENOME SCI

PRINCIPIA PHARM CORP.

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                                                             MKISVAAIPFFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
                                             1 MKISVAAIPPFLLITIALGTKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCS
                       Gaps
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                                                                                                                                                                                                                                                                         albumin fusion protein; albumin activity; human serum albumin; serum osmotic pressure; shelf-life; stability; antidiabetic; gene therapy; diabetes mellitus; human; gene; ds.
                       Indels
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          Pred. No. 1e-52;
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                                                                                           KPGIVFITKRGHSVCTNPSDKWVQDYIKDMKEN
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                       Mismatches
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100.0%; Pre-
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27-MAR-2002; 2002US-0367500P.
08-APR-2002; 2002US-037500P.
10-MAY-2002; 2002US-0378950P.
24-MAY-2002; 2002US-03182617P.
28-MAY-2002; 2002US-038123P.
05-JUN-2002; 2002US-038173P.
05-JUN-2002; 2002US-0385708P.
10-JUL-2002; 2002US-0389808P.
09-AUG-2002; 2002US-0402131P.
                                                                                                                                                                              ADF15204 standard; protein; 93
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DELTA BIOTECHNOLOGY L
PRINCIPIA PHARM CORP.
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18-SEP-2002; 2002US-0411426P.
02-OCT-2002; 2002US-0414984P.
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2002US-0351360P.
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2002US-0420246P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating diabetes mellitus
                                                                                                                                                                                                                           (first entry)
          Similarity 100.
93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ballance DJ, Turner AJ,
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05-NOV-2002;
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          Best Local
Matches 9
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(PRIN-)
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                                                                                                                                                       RESULT 30
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functions as a carrier of endogenous and exogenous ligands. The fusion of albumin to a therapeutic protein may increase shelf-life and stability of the therapeutic protein. The albumin fusion protein of the invention may allow production of compositions with antidiabetic activity whilst the nucleotide sequence which encodes it may be useful for gene therapy. The albumin fusion protein is useful for preparing a composition for treating diabetes mellitus. The present sequence is that of a therapeutic protein which was fused with human albumin to create a novel albumin fusion protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
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